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Result
No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               Score
                                                                             58.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            February 6, 2003, 21:34:44; Search time 36 Seconds (without alignments) 151.758 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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1: /SIDS2/gcgda+>/
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                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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ABP38752
AAG82688
ABP39600
AAG09408
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AAG09406
AAU53139
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Compugen Ltd.
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Staphylococcus epi
S. epidermidis ope
Staphylococcus epi
Arabidopsis thalia
Arabidopsis thalia
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 C
                         Propionibacterium
              Lactococcus lactis
glutamicum prote
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AAM52607
 Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                              AAM52607 standard; Protein; 41 AA
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                                                                                                                                                                                                                                                                                                                                                                      AAM52607;
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49	4 4	4.	49	49	49	49	49	49.5	49.5	49.5	49.5	49.5	50	50	50	50	50	50.5	50.5	51	51	51	51	51	51	51	51.5	52	52	53.5	53.5	53.5	54
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390	258	102 102	154	146	146	137	103	1024	909	551	240	97	578	265	265	248	232	491	355	1360	817	799	567	541	404	86	294	459	455	206	206	206	1048
11	21	2 2	22	23	21	21	21	23	22	23	23	22	22	18	11	22	21	23	22	22	21	21	21	23	23	20	22	22	22	22	22	21	22
AAR05475	AAG33209	AAG33210	ABB62506	ABB91722	AAG05688	AAG33211	AAG05689	ABB07504	AAU03554	ABP29598	ABB92584	AAU49588	ABB57874	AAW14464	AAR06909	AAU30985	AAB38330	ABP38665	ABB57739	ABB61753	AAB24965	AAB24966	AAB24967	ABB49247	ABB95184	AAY34616	ABB67023	ABB67668	AAU64449	AAU37083	AAU34255	AAB11050	ABG20939
oramphenicol r	Arabidopsis thalla	Zea mays protein t	Drosophila melanog	Herbicidally activ	is thali	Zea mays protein f	Arabidopsis thalia	Human GTP-binding	Human protein kina	Streptococcus poly	Herbicidally activ	Propionibacterium	Drosophila melanog		Intra-acrosomal sp		Human secreted pro	Staphylococcus epi	Drosophila melanog	Drosophila melanog				Listeria monocytog	Human 158P1H4 spli	Chlamydia pneumoni	Drosophila melanog	Drosophila melanog	Propionibacterium	Staphylococcus aur	Staphylococcus aur	Staphylococcus aur	Novel human diagno

ALIGNMENTS

Beta-lactam resistance; blr gene; Beta Lactam-358; BLR; transmembrane; efflux pump; periplasm; peptidoglycan synthesis inhibition; drug discovery; screening; antibiotic; antibacterial; vaccine; Levy SB, McMurry LM 06-APR-2000; 2000US-195505P 14-JUL-2000; 2000US-218380P 18-OCT-2001. Escherichia coli. gene therapy Escherichia coli beta-lactam resistance (BLR) (TUFT) TUFTS COLLEGE 06-APR-2001; 2001WO-US11363 WO200177176-A2 6. Location/Qualifiers /label= Transmembrane_domain protein.

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RESULT 2
ABP3752
ID 38P3
XX ABP3
AC AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a beta-lactam resistance (BLR) protein from CC Escherichia coli. The BLR protein is a 41 amino acid transmembrane CC protein (also designated Beta Lactam-358 in the specification) with a CC molecular weight of 4556 Daltons which confers resistance to beta-lactam antibiotics. The blr gene which encodes it was initially identified in a CC 602 bp hypothetical intergenic region of the genome of an antibiotic-cC susceptible strain of E. coli, RW383. In the RW583 strain, the blr gene cC is disrupted by insertion of the transposon mini-TnphoA. A clone bearing cC region was found to restore beta-lactam resistance in RW358. Certain CC amber suppressor, indicating that a protein encoded by the clone was counted to amber suppressor, indicating that a protein encoded by the clone was responsible for mediating beta-lactam resistance. It is suggested that the BLR protein may act by increasing a beta-lactamase activity in a CC cell, possibly being a component of an uncharacterised membrane-bound cC efflux pump capable of expelling beta-lactams from the periplasm. The BLR protein may be used in methods to identify compounds that modulate antibutic resistance in a bacterium. The BLR protein, gene, BLR protein bacterial infection, particularly by an organism resistant to antibutics that affect peptidoglycan synthesis. They may also be used to treat bacterial infection, particularly by an organism resistant cc used in screening assays, in vaccines, and in diagnostic assays. BLR CC expression, and to detect BLR expression in a biological sample.
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Best Local
(GENO-) GENOME THERAPEUTICS CORP
                                                                  14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                           US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus antibacterial;
                                                                                                                                                                 13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP38752 standard; Protein; 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New membrane protein, designated Beta Lactam-358 polypeptides, that affect susceptibility to antibiotics which affect peptidoglycan synthesis in microbes, useful for identifying modulators for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABA02070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  epidermidis; open reading frame; ORF; bacterial infection; gene therapy.
                                                              97US-055779P.
97US-064964P.
                                                                                                                                                              98US-0134001
                                                                                                                                                                                                                                                                                                                                                          epidermidis
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Pred. No. 1.2e-21;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                             Claim 18;
                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                          N-PSDB;
                                                                                                                                     WPI; 2001-316495/33.
                                                                                                                                                               Kimmerly WJ;
                                                                                                                                                                                        (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                 09-NOV-1999;
                                                                                                                                                                                                                                         09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                    17-MAY-2001.
                                                                                                                                                                                                                                                                                          WO200134809-A2
                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                            vaccination;
                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                  S. epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a polypeptide, useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GWIVLVVSVILLGVA-----SHID--NYQPPEQSASVQHK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIIIFIISVIITGVSALRDKSHEDRQNQRPNQKTSNEQHQ 47
                                                                                                                           AAH53538.
                                                         Page 651; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 3597;
                                                                                                                                                                                                                                                                                                                                            endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                  epidermidis
                                                                                                                                                                                                                                                                                                                                                                               open reading
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                    SR1 strain; infection; diagnosis,
                                                                                                                                                                                                                                                                                                                                                                               frame protein sequence SEQ ID NO: 2470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.5; D
Pred. No. 2.5;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the

AAH52304 to

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RESULT 4
ABP396000
ID ABP3
XX ABP3
XX ABP3
XX Stag
XX 
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CC N.B. The present invention specifically claims all the polynucleotide CC sequences given in the sequence listing of the present specification, CC however the sequence listing only goes up to SEQ ID NO:4454 So even CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, con sequences are present for SEQ ID NO:4465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The s. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding a polypeptide, useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN92145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 - JUL - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP39600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP39600 standard; Protein; 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ហ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRLITLIG-VLLIILAIYLFSKPYIDNY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 AA;
                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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97US-064964P
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                                                                                                                                                                                                                                                                                                                                                                   ID 4445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bush D;
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Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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RESULT 5
AAG09408
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Best Local
23-APR 1999
23-APR 1999
28-APR 1999
30-APR 1999
30-APR 1999
04-MAY 1999
05-MAY 1999
06-MAY 1999
07-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                         25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

11-APR-1999

11-APR-1999

21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic hwhridisation assav: genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG09408 standard; Protein; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                               termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 7330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG09408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNRLIELTGWIVLVVSVILLGVASHIDNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRLITLIG-VLLIILAIYLFSKPYIDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
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                                                                                                                                                                                                                                                                                                                                                                    2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
99US-0134941.
99US-0135124.
99US-0135353.
99US-0135629.
99US-0136021.
99US-0136782.
99US-0137722.
99US-01377528.
                                                                                   99US-0132863.
99US-0134256.
99US-0134218.
99US-0134219.
99US-0134221.
99US-0134370.
99US-0134768.
                                                                                                                                                     99US-0132484.
99US-0132485.
99US-0132486.
99US-0132487.
                                                                                                                                                                                           99US-0131449.
99US-0132048.
99US-0132407.
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99US-0130077
                                                                                                                                                                                                                        990S-0130510.
990S-0130891.
                                                                                                                                                                                                                                                                                         99US-0126785
99US-0127462
                                                                                                                                                                                                                                                                                                                                                 99US-0121825
                                                                                                                                                                                                                                           99US-0130449
                                                                                                                                                                                                                                                                       99US-0128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.3%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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promoter;
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00-JUN-1999
00-JUN-1999
00-JUN-1999
10-JUN-1999
11-JUN-1999
11-JUN
990S-0137502.
990S-0138540.
990S-0138094.
990S-0138044.
990S-0139453.
990S-0139453.
990S-0139455.
990S-0139457.
990S-0139457.
990S-0139457.
990S-0139457.
990S-0139460.
990S-0139460.
990S-0139460.
990S-0139463.
990S-014053.
990S-014083.
990S-014083.
990S-014083.
990S-014083.
990S-014083.
990S-0144884.
990S-014528.
990S-014538.
990S-014538.
990S-0147204.
990S-0147204.
990S-0147204.
990S-0147204.
                                                     Query Match
Best Local
                                                06-AUG-1999
06-AUG-1999
09-AUG-1999
10-AUG-1999
11-AUG-1999
12-AUG-1999
12-AUG-1999
13-AUG-1999
13-AUG-1999
14-AUG-1999
14-AUG-1999
15-SEP-1999
16-SEP-1999
16-SEP-1999
17-AUG-1999
18-AUG-1999
18-AUG
    Similarity
                                                  99US-0147303.
99US-01474935.
99US-01487416.
99US-0148341.
99US-0148341.
99US-0148341.
99US-0148341.
99US-0149368.
99US-0149368.
99US-0149368.
99US-0149369.
99US-0149929.
99US-0150566.
99US-0151066.
99US-0151066.
99US-0151068.
99US-0151068.
99US-0151068.
99US-0151068.
99US-0151069.
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99US-0155488.
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99US-0155488.
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99US-0155488.
99US-0155488.
99US-0155488.
99US-015933.
99US-015933.
99US-015933.
99US-0159638.
99US-0159638.
99US-016076.
99US-016076.
99US-016076.
99US-0160815.
99US-0161363.
99US-0161363.
99US-0161369.
99US-0161369.
99US-0161369.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161361.
        28
34
        . 0%;
        Score
Pred.
        58;
         7.3;
                      21;
                        Length
                         291;
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PR 16-JUN-19 PR 18-JUN-19 PR 28-JUN-19 PR 28-JUN-19 PR 28-JUN-19 PR 28-JUN-19 PR 28-JUN-19 PR 28-JUN-19 PR 18-JUN-19 PR 18-JUN-19 PR 28-JUN-19 PR 18-JUN-19 PR 28-JUN-19 PR 28	14-MAY-1999; 991 14-MAY-1999; 991 18-MAY-1999; 991 19-MAY-1999; 991 21-MAY-1999; 991 21-MAY-1999; 991 24-MAY-1999; 991 25-MAY-1999; 991 27-MAY-1999; 991 27-MAY-1999; 991 27-MAY-1999; 991 27-JUN-1999; 991 07-JUN-1999; 991 07-JUN-1999; 991 10-JUN-1999; 991	PR 05-FEB-1999; 99US-0123180. PR 09-MAR-1999; 99US-0123548. PR 23-MAR-1999; 99US-0125788. PR 23-MAR-1999; 99US-0126785. PR 25-MAR-1999; 99US-0126785. PR 01-APR-1999; 99US-0128734. PR 06-APR-1999; 99US-0128734. PR 16-APR-1999; 99US-0130477. PR 119-APR-1999; 99US-0130477. PR 21-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130449. PR 28-APR-1999; 99US-0130449. PR 28-APR-1999; 99US-013048. PR 04-MAY-1999; 99US-0132486. PR 05-MAY-1999; 99US-0132486. PR 06-MAY-1999; 99US-0132486. PR 11-MAY-1999; 99US-01334256. PR 11-MAY-1999; 99US-01334256. PR 11-MAY-1999; 99US-01334218.	SULT 6 G09407 AAG09407; AAG09407; 17-OCT-2000 (firs Arabidopsis thalia Protein identifica hybridisation assatermination sequer Arabidopsis thalia EP1033405-A2. 06-SEP-2000; 25-FEB-2000; 20001	Matches 10; Conservative 10; Mismatches 9; Indels 0; Gaps 0; Qy 3 RLIELTGWIYLVVSVILLGVASHIDNYQP 31 : : :::: : : : Db 212 RLLLLLGWLLIMLGVVLLVTSSRLIRHLP 240
	27 JUL 28 JUL 28 JUL 28 JUL 27 JUL 28 JUL 27 JUL 28 JUL 27	13-Jun- 15-Jun- 16-Jun- 16-Jun- 19-Jun- 19-Jun	18 JUN 18	R 16-JUN-1 R 17-JUN-1 R 18-JUN-1 R 18-JUN-1

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Query Match
Best Local S
Matches 10
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16-AUG-1999
17-AUG-1999
18-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
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21-AUG-1999
22-AUG-1999
23-AUG-1999
24-AUG-1999
27-AUG-1999
27-AUG-1999
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27-AUG-1999
27-AUG-1999
27-AUG-1999
28-EEP-1999
29-EEP-1999
20-EEP-1999
21-AUG-1999
21-AUG-1999
21-AUG-1999
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26-AUG-1999
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25-AUG-1999
26-AUG-1999
27-AUG-1999
28-AUG-1999
28-AUG-1999
29-AUG-1999
21-AUG-1999
21-AUG
                                         ch 28.0%;
l Similarity 34.5%;
10; Conservative
                                                                                                                                                                                                                             99US-0148565.
99US-0149175.
99US-0149175.
99US-0149723.
99US-0149723.
99US-0149923.
99US-0150884.
99US-0151065.
99US-0151303.
99US-0155753.
99US-0158029.
99US-0158029.
99US-0158029.
99US-0159331.
99US-0159331.
99US-0159331.
99US-0159331.
99US-0160741.
99US-0160768.
99US-0160768.
99US-0160989.
99US-0161160.
99US-0161161.
                                                                                                                                       10;
                                                                                                                                       Score 58; DB 2
Pred. No. 8.9;
10; Mismatches
                                              293
                                                                                        31
                                                                                                                                                                                      21;
                                                                                                                                            9;
                                                                                                                                                                                 Length 344;
                                                                                                                                          Indels
                                                                                                                                          0;
                                                                                                                                          Gaps
                                                                                                                                          0
RESULT 7
AAGOVACA
ID AAGOVACA
AACOVACA
AAGOVACA

25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
26-AAR-1999
06-APR-1999
06-APR-1999
07-APR-1999
08-APR-1999
08-APR
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG09406;
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99US-0121825.
99US-0125788.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0130449.
99US-0133486.
99US-0132486.
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99US-0132486.
99US-0132486.
99US-0132486.
99US-0134218.
99US-0134218.
99US-013421.
99US-013421.
99US-013422.
99US-013422.
99US-013422.
99US-013422.
99US-013422.
99US-01342.
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RESULT 8
AAU53139
ID AAU5
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AC AAU5
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AC 27-F
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                                                                                                                                          Query Match 28.0%;
Best Local Similarity 34.5%;
Matches 10; Conservative 1
                                                                                                                                       23-SEP 1999
24-SEP 1999
28-SEP 1999
29-SEP 1999
04-OCT 1999
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                 AAU53139;
                                 AAU53139 standard;
27-FEB-2002 (first entry)
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                                 Protein;
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                                 327
                                                                                                       Score 58; DB
Pred. No. 9.4;
10; Mismatches
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                                                                                                                         DB
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                                                                                                                       Length 361;
                                                                                                         Indels
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-JUL-1999; -JUL-1999; -JUL-1999; -JUL-1999; -JUL-1999;

-JUL-1999

-1999; -1999; -1999;

-JUL-1999 -JUL-1999

Propionibacterium acnes immunogenic protein #14035

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RESULT 9
ABB54920
ID ABB5
XX
AC ABB5
XX
DT 16-M
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                                                                                                                                                                                                                                                                                   sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. p. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of p. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for p. acnes proteins. These antibodies can be used to therefore treat p. acnes infections. The antibodies may also be used as diagnostic agents for determining p. acnes presence, for example, by
                                                                                                                                                              Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes vaccinating against and treating acne vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes
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   16-MAY-2002
                          ABB54920;
                                                  ABB54920
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                     specification,
                                                                                                                                                                                                                                                                             enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID No 14334;
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                                                                                                              249
                                                                                                                                                              Local Similarity 45.
                                                                                                                                       7
                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                              LAGWLVIVTGGLEAGVAAHVVN
                                                                                                                          LTGWIVLVVSVILLGVASHIDN
                                                                                                                                                                                                                                                   e linked immunosorbent assay (ELISA).

The sequence data for this patent did not form fication, but was obtained in electronic format
                                                  standard;
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e J, Zhang Y,
  (first entry)
                                                                                                                                                                                                                A,
                                                  Protein;
                                                                                                                                                                           27.5%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069pp; English.
                                                                                                                 270
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Pred.
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                                                                                                                                                                                       Length 327;
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are used in
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleotide sequence useful in the identification or Lactococcus lactis and related species \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000;
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                                                                                      Sequence
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l Similarity
11; Conserv
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    Conservative
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                      26.6%;
37.9%;
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    8,
                         Score 55;
Pred. No.
      Mismatches
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                    DВ
21;
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                                             Length 320;
         0,
         Gaps
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Query Match Best Local S Matches 11 ш 1 MNRLIELTGWIVLVVSVILLGVASHIDNY 29 MKKRKKMIAWILVVLSVVLVGGYFAIGNY 29 0

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RESULT 10 AAG92354 ID AAG92

AAG92354 standard; Protein; 900 A

AAG92354;

26-SEP-2001 (first entry)

C glutamicum protein fragment SEQ ID NO: 6108

Coryneform bacterium; a organic acid synthesis. amino acid synthesis; vitamin;

Corynebacterium glutamicum

20-JUN-2001.

18-DEC-2000; 2000EP-0127688

PR R F F D XXX 16-DEC-1999; 07-APR-2000; 03-AUG-2000; 99JP-0377484. 2000JP-0159162. 2000JP-0280988.

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RESULT 11
ABG20939
ID ABG20
XX ABG20
XX ABG20
XX ABG20
XX HOWel
XX Homan
KW Food
XX Homo
XX HO
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European patent of fice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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New isolated polynucleotide and encoded polypeptides, useful
                                                             N-PSDB; AAS85126
                                                                                     WPI; 2001-639362/73
                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #20930
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nes 13; Conserv
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                                                                                                                                               Liu C,
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Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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da M, Ozaki A;
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Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                              CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in itssue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical cimaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (III) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC dispossible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.
                                              Best Loc
Matches
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20;
                                                                                                                                     Sequence
                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                      Local
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 51298; 103pp; English
                                                                                                                                        1048
                                                 Conservative
                                                                                                                                        AA;
                                                                    26.1%;
                                            9;
                                                                    Score 54; DB 22;
Pred. No. 1.2e+02;
                                            Mismatches
                                            8,
                                                                                         Length 1048;
                                            4;
                                            Gaps
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RESULT 12
AAB11050
                                                                                                                                                                                                                                             peptidoglycan; antibacterial;
bacterial infection.
                                                                                                                                                                                                                                                                                                                Staphylococcus aureus sortase transamidase srtA protein.
Schneewind O,
                                                                                                      13-APR-2000; 2000WO-US10198
                                                                                                                                       26-OCT-2000
                                                                                                                                                                           WO200062804-A2
                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                Sortase transamidase; Gram-positive bacterium; covalent cross-link;
                                                                                                                                                                                                                                                                                                                                                    16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11050 standard; Protein;
                                  (REGC ) UNIV CALIFORNIA
                                                                    15-APR-1999;
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Mazmanian
                                                                      99US-0292437
                                                                                                                                                                                                                                                                                                                                                                                                                       206
Liu
                                                                                                                                                                                                                                                               vaccine; treatment; detection; srtA;
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e,
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A substantially purified sortase-transamidase from a ${\tt Gram-positive}$ bacterium for use in the treatment and detection of ${\tt Gram-positive}$ bacterial infections -

WPI; 2000-665197/64. N-PSDB; AAC65625.

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Best Local
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                                                                                                                                                                                                                                                    21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus cellular proliferation protein #531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU34255
  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                     New polynucleotides for the identification and antibiotics, comprise sequences of antisense nu
                                                                                                                          WPI; 2001-611495/70.
N-PSDB; AAS52114.
                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                                                                                                                                                               WO200170955-A2
                                                                Example
                                                                                                                                                                  Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                               16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              prokaryotic cellular proliferation protein
; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                  Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                        aureus
                                                                ID No 5751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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 encoded proteins.
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                                                             511pp;
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Pred.
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                                                              English
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                                                                                        nucleic
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ucleic acids
 prokaryotes
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RRESULT 14
AAUJ7083
AID AAUJ7083
AID AAUJ7083
AID AAUJ7083
AID AAUJ7083
AID Stap
XXX ANL1
KW ANL1
KW ANL1
KW ANL1
KW ANL1
KW ANL1
COS Stap
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XXX STAP

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                    New polynucleotides antibiotics, compris
                                                                                                                                                                                                                                                                                                                            Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus cellular proliferation protein #1253.
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16-FEB-2001;
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                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                    ELITRA PHARM
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                                                                                                                        Seq ID
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                            comprise sequences
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2001US-269308P
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Xu HH;
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                                                                                                                           No 12676;
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                                                                                                                        511pp;
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Pred. No. 21
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                                                                                                                              English.
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RESULT 15
AAU64449
ID AAU64449
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XX AAU64
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XX AAU64
XX SAPH
KW SAPH
KW Uvei
KW Infi
KW dern
XX Pro
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-616774/71.
N-PSDB; AAS59644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes immunogenic protein #25345
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                                                                                                                                                                                   Example 1; SEQ ID No 25644; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                 acne vulgaris
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ve J, Zhang 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 455
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitcham JL, Wang SS,
, Jen S, Carter D;
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Pred. No. 21;
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Best Local :
                                                                                                                                                                                                                                polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                            P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                          and determining the amount of bound protein in the sample. The
                                                                                                                                                                         Sequence
163 EMEFWFAMIKIVTIIALILVGGYLAITGFQPPRSGVPAASFSH
                                         6 ELTGW-----IVLVVSVILLGVASHIDNYQPPEQ----SASVQH
                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                        14;
                                                                                                         Similarity
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                                                                                      Conservative
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                                                                                                         25.1%;
                                                                                      8
                                                                                                         Score 52; DB Pred. No. 85;
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                                                                                                                             22;
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Search completed: February Job time: 38 secs 0 2003, 21:38:14

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Maximum
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                           US-09-398-395A-52

US-09-134-001C-4442

US-09-123-365-74

US-09-515-039-74

US-09-515-039-74

US-09-134-001C-3771

US-08-706-936-2

US-08-706-936-2

US-08-616-844-39

US-08-944-868A-39

US-08-944-868A-39

US-08-944-423A-39

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US-09-510-949-2
US-09-134-001C-5667
US-09-601-091-2
US-09-601-091-4
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US-09-134-001C-4445

US-08-292-045-10

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10, Appl
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 LENGTH: 203
TYPE: PRT
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US-08-023-610-6	US-08-663-566A-6	US-08-487-596-16	US-09-134-001C-4109	US-09-134-001C-4900	US-09-134-001C-4165	US-08-001-554A-4	US-08-467-961A-4	US-08-467-969A-4	US-08-987-439-3	US-08-344-639E-4	US-08-852-344D-4	US-08-838-189D-4	US-08-467-963C-4	US-09-457-046B-52	US-09-457-046B-14	US-08-549-515-10	US-08-908-643C-51
Sequence 6, Appli	Sequence 6, Appli	Sequence 16, Appl	Sequence 4109, Ap	Sequence 4900, Ap	Sequence 4165, Ap	Sequence 4, Appli	4,	Sequence 4, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 52, Appl	Sequence 14, Appl	Sequence 10, Appl	Sequence 51, Appl

ALIGNMENTS

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RESULT 1

(S-09-134-001C-3597, Application US/09134001C)

Sequence 3597, Application US/09134001C

Patent No. 6380370

(GENERAL IMPORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: UUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: GTC-007

(CURRENT APPLICATION NUMBER: US/09/134,001C

(CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3597

LENGTH: 231
TYPE: PRT
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3597
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-134-001C-4445; App.
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: COLDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PILLORION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR RILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4445
                                                                                                                                                                                                                                                                                                                                         Patent No. 6380370
GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conserv
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US-09-134-001C-3510
               RESULT 4
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Best Local
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/318,551
FILING DATE: 03-MAR-1989
APPLICATION NUMBER: US 07/481,491
FILING DATE: 16-FEB-1990
APPLICATION NUMBER: US 07/858,798
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5602005man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 494-109-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                          TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HERR, JOHN C.
APPLICANT: WRIGHT, RICHARD M.
TITLE OF INVENTION: POR USE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                 Local Similarity 36.0
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                                                                 MNRFL----
                                                                                                                                                                                                                                           amino acids
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                 --LLMSLYLLGSARGTSS-QPNESSGSIDHQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR USE IN A CONTRACEPTIVE VACCINE 29
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                                                                                                                                               Score 52; DB 1;
Pred. No. 7.1;
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SEQ ID NO 3510
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Best Local Similarity
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TYPE: PRT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 VLVVSVILLGVAS-----HIDNYQPPEQSAS----VQHK 41
                                                                                                                                            APPLICATION NUMBER: US 07/318,551
FILING DATE: 03-MAR-1989
APPLICATION NUMBER: US 07/481,491
FILING DATE: 16-FEB-1990
APPLICATION NUMBER: US 07/858,798
FILING DATE: 27-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
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TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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               TELEFAX:
                                 TELEPHONE:
                                                                        REFERENCE/DOCKET NUMBER:
                                                                                          REGISTRATION NUMBER:
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5. 5602005
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Y: U.S.A.
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                                   (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jefferson Davis Highway, Suite 400
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Pred. No. 23;
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INFORMATION FOR SEQ ID NO:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-922-865-2
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US-08-922-865-2
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                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09510949 Patent No. 6423522
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                             FILING DATE:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2 COMPUTER READABLE FORM:
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               SEQUENCE CHARACTERISTICS:
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                                                                                           APPLICATION NUMBER: US/09/510,949 FILING DATE:
                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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575 amino acids
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Pred. No. 55;
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5667
LENGTH: 309
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5667
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MOLECULE TYPE:
US-09-510-949-2
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; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-601-091-2
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APPLICANT: COLby, S. M. et al.
TITLE OF INVENTION: Germacrene C Synthase
FILE REFERENCE: 4630-55758
CURRENT APPLICATION NUMBER: US/09/601,091
CURRENT FILING DATE: 2000-09-19
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                                                                                                                                                                                                 SEQ ID NO 2
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Best Local
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Matches 13; Conserv
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Best Local
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                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR FILING DATE: 1998-02-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US99/02133 PRIOR FILING DATE: 1999-02-02
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                              11 IVLVVSVILLGVASHIDNYQPPEQSASVQH 40
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LVLIDAMQRLGVAYHFDN----EIETSIQN 86
                                                                12;
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Pred. No. 55;
                                                                6; Mismatches
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                                                                               Score 46; DB 4;
Pred. No. 1.2e+02
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Pred. No.
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APPLICANT: Chappell, Joseph P.
APPLICANT: No. 64687721, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION UNMBER: U5/09/398,395A
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 548
TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-601-091-4
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US-09-398-395A-52
US-09-398-395A-52
: Sequence 52, Application US/09398395A
: Patent No. 6468772
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                                       RESULT 12
US-09-134-001C-4442
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TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-09-398-395A-52
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APPLICANT: COlby, S. M. et al.
APPLICANT: COlby, S. M. et al.
TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon Esulentum
FILE REFERENCE: 4630-55758
CURRENT APPLICATION NUMBER: US/09/601,091
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: PCT/US99/02133
PRIOR APPLICATION NUMBER: PCT/US99/02133
PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR FILING DATE: 1998-02-02
Sequence 44 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09601091 Patent No. 6342380
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-01
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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Local Similarity 40.0%;
nes 12; Conservative
                                                                                                                               61 LVLIDAMQRLGVAYHFDN----EIETSIQN 86
                                                                                                                                                                      11 IVLVVSVILLGVASHIDNYQPPEQSASVQH 40
  4442, Application US/09134001C
5. 6380370
                                                                                                                                                                                                            22.2%;
milarity 40.0%;
Conservative
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1999-08-23
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02
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                                                                                                                                                                                                                                                          DB 4;
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GENERAL INFORMATION:
APPLICANT: Natori, Shunji
FILLE OF INVENTION: NEW PROTEASE
FILL REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER APPLICATION NUMBER: UP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Vigna mungo CP US-09-120-365-74
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US-09-120-365-74
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US-09-515-039-74
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CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Applica Patent No. 6103514 GENERAL INFORMATION:
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SEQ ID NO 4442
LENGTH: 249
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Best Local 9
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                                   SOFTWARE: P
SEQ ID NO 74
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
TYPE: PRT
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                  LENGTH: 362
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Local Similarity 31.4%;
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                                                     PatentIn Ver. 2.0
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34.3%; Pred. No. 86;
Live 10; Mismatches
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Pred. No. 54;
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RESULT 15

(S-09-134-001C-3771
(Sequence 3771, Application US/09134001C
(Patent No. 6380370
(GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: LYnn DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
(TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
(TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
(TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
(TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
(FILE REFERENCE: GTC-007
(CURRENT APPLICATION UNMBER: US/09/134,001C
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Search completed: February 6, 2003, 21:39:54 Job time: 17 secs
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.0%; Score 45.5; DB 4; Length 456; Best Local Similarity 27.5%; Pred. No. 1.1e+02; Matches 11; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                            149 ELEFWFAIKIVTIIALIVIGVIMILFAFKTPFGNTSLTH 188
                                                                                                                                                                                                                                                                                  6 ELTGW-----IVLVVSVILLGVASHIDNYQPPEQSASVQH 40
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                    seq length:
seq length:
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length: 2000000000
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        129505 seqs,
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                                                                                                                                                                                                                                                                                                                       Match
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Copyright (c) 1993 - 2003 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-09-738-626-6108
US-09-933-999A-3
10 US-09-815-242-5751
10 US-09-815-242-12676
10 US-09-815-242-13676
10 US-09-918-295A-330
US-09-978-192A-330
US-10-123-94-272
US-10-123-944-272
                     US-09-815-242-12011
US-09-738-626-5932
US-10-033-109-10
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Sequence 2, Appli
Sequence 5108, Ap
Sequence 31, Appli
Sequence 5751, Ap
Sequence 12676, A
Sequence 5136, Ap
Sequence 330, App
Sequence 330, App
Sequence 330, App
Sequence 330, App
Sequence 272, App
Sequence 273, App
Sequence 5932, Ap
Sequence 5932, Ap
Sequence 5932, App
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US-09-828-456-2
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US-09-828-456-2
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Matches
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LENGTH:
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                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Levy, Stewart et al.

TITLE OF INVENTION: No. US20020051982A1el BLR Molecules Affecting Antibiotic Susce
FILE REFERENCE: PKZ-030

CURRENT APPLICATION NUMBER: US/09/828,456

CURRENT FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,505
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/218,380
PRIOR FILING DATE: 2000-07-04
NUMBER OF SEQ ID NOS: 2
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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ALIGNMENTS

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RESULT 2
US-09-738-626-6108

Sequence 6108, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
   APPLICANT:
                                                          APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                       h 100.0%; Score 207; DB 10; Similarity 100.0%; Pred. No. 1.5e-21; 41; Conservative 0; Mismatches 0;
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
                                            SEIKO
                                                          HIROSHI
                                                                                                                                                                                                                                                                           Length 41;
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                                                                                                                                                                                                                                                Gaps
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APPLICANT:

TATEISHI, NAOKO SENOH, AKIHIRO

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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6108
LENGTH: 900
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US-09-815-242-5751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/933,999A
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 206
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Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09933999A Publication No. US20030022178A1
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                                                                                                                                                              GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT: Schneewind et al.
TITLE OF INVENTION: Identification of Sortase
FILE REFERENCE: 510015-249
                                                                   APPLICANT:
                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Karl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 206
TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: IKEDA, MASATO PPLICANT: OZAKI, AKIO
ITLE OF INVENTION: Identification of Essential Genes in
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                                                                                                                                                                                                                                                                                               NRLMTIAG-VVLILVAAYLFAKPHIDNY 32
                                                                                                                                                                                                                                                                                                                                 NRLIELTGWIVLVVSVILLGVASHIDNY 29
                                                                   Wall, Daniel
Trawick, John D.
                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
                              Carr, Grant J.
Yamamoto, Robert T.
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Pred. No. 4.4;
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Pred. No. 18;
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                                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5751
LENGTH: 206
                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12676
LENGTH: 206
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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ORGANISM: Staphylococcus aureus
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Zyskind, Judith W.
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42.9%;
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Pred. No. 4
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US-09-978-295A-330

Sequence 330, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:
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US-09-815-242-5136
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SEQ ID NO 5136
LENCTH: 1053
TYPE: PRT
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Best Local
                                                                   APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
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                                    APPLICANT:
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   APPLICANT:
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400 LVLSIGIVVDDAIVVVENVERHIENGEPPLQAA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-11-27
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12; Conserv
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Zyskind, Judith W.
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
                                                     Eaton, Dan
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Yamamoto, Robert T.
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; Pred. No. 1.2e
7; Mismatches
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Pred. No. 4.
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PRIOR FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/077649
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
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Grimaldi, J. Christopher
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Kuo, Sophia S.
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Hillan, Kenneth J
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APPLICATION NUMBER: 60/080328 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080333

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FILING DATE: 1998-04-01
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DR APPLICATION NUMBER: 60/081049
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DR APPLICATION NUMBER: 60/081071
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DR APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-09
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DR APPLICATION NUMBER: 60/08129
DR FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/084637
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FILING DATE: 1998-05-13
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Desnoyers, Luc
Eaton, Dan
Ferrar
                                    Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                     Ashkenazi, Avi
Baker Kevin P
                                                                                       Fong,
                                                                                                     Ferrara, Napoleon Filvaroff, Ellen
          Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Stewart, Timothy A.
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Kljavin, Ivar J.
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ms, P. Mickey
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APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07

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APPLICATION NUMBER:

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Baker Kevin P.
Botstein, David
                                                                                                                                                                                                                                                      Fong,
               Pan, J
                                                                                                                                             Godowski, Paul J.
Grimaldi, J. Christopher
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Gerber, Hanspeter
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Nicholas F
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PRIOR FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/081071

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     TITLE OF INVENTION:
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TGWIV---LVVSVILL-----GVASHIDNYQPPEQ
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APPLICATION NUMBER: 60
FILING DATE: 1998-05-1
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/
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                                                                                                                                 Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                     Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                       Williams, P. Mic
Wood, William I.
                                                                                                        Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker Kevin
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                                                                                                                                                                                                                                                                        Napier,
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                                                                                                                                                                                                                                               James;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dan
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                                                                                                                                                                                                                                                                  Mary A.
Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Napoleon
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                                                                                  Mickey
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Pred. No. 35;
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APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: 60 FILING DATE: 1998-04-APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22

60/082797 60/082700 60/082804 FILING DATE: 1998-04-2 APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE: 1998-04-2 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-15 FILING DATE: 1998-04-15

60/082569

FILING DATE:

1998-04-22

60/082704

FILING DATE:

1998-04-27

60/083322

APPLICATION NUMBER:

APPLICATION NUMBER: 60/083392

PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER:

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

FILING DATE: 1998-04-29 APPLICATION NUMBER:

PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-0 APPLICATION NUMBER:

APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-04-29

60/083742 60/083500 60/083559 60/083558 60/083554

1998-04-29

FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0

1998-05-06

60/084414

1998-05-05 1998-04-30

60/084366

FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

APPLICATION NUMBER: 60/084441 FILING DATE: 1998-05-06

APPLICATION NUMBER: FILING DATE: 1998-0

APPLICATION NUMBER: 60/084639 FILING DATE: 1998-05-07

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FILING DATE:

1998-04-29

60/083545

APPLICATION NUMBER:

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APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

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FILING DATE:

1998-04-29 1998-04-29 1998-04-29

60/083499

60/083496 60/083495

OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064249
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077641
OR APPLICATION NUMBER: 60/077641
OR FILING DATE: 1998-03-11

FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30 PRIOR OR APPLICATION NUMBER: 60/083554
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083558
OR APPLICATION NUMBER: 60/083558 OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/08336
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083392
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083495
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OR APPLICATION NUMBER: 60/083496
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OR APPLICATION NUMBER: 60/083499
OR APPLICATION NUMBER: 60/083545 DR APPLICATION NUMBER: 60/082704
DR FILING DATE: 1998-04-22
PR APPLICATION NUMBER: 60/082804
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082700
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082797
DR APPLICATION NUMBER: 60/082797 DR FILING DATE: 1998-05-06
PREFIZION NUMBER: 60/084441
DR APPLICATION NUMBER: 60/084637
DR APPLICATION NUMBER: 60/084639
DR APPLICATION NUMBER: 60/084640
DR APPLICATION NUMBER: 60/084640
DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084598
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DR FILING DATE: 1998-05-07
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DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30
DR APPLICATION NUMBER: 60/084366
DR FILING DATE: 1998-05-05
DR APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-21 FILING DATE: 1998-04-1 APPLICATION NUMBER: 60 FILING DATE: 1998-04-1 APPLICATION NUMBER: FILING DATE: 1998-0.
APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 FILING DATE: APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796 FILING DATE: APPLICATION NUMBER: 1998-04-21 1998-04-1 1998-04-1 1998-04-09 1998-04-: 60/081838)4-15 60/082568 60/081817 60/082569 60/081955 60/081952 60/081819

DR APPLICATION NUMBER: 60/078910
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078939
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25

FILING DATE: 1998-03-20 APPLICATION NUMBER:

1998-03-20

60/078936

APPLICATION NUMBER:

APPLICATION NUMBER:

1998-03-27

1998-03-27

60/079920

60/079786 60/079728 APPLICATION NUMBER: FILING DATE:

NUMBER: 60/079663 1998-03-27

1998-03-1998-03-27

60/079689

APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664

OR APPLICATION NUMBER: 60/077649
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
OR APPLICATION NUMBER: 60/0780886
OR APPLICATION NUMBER: 60/078886

PRIOR PRIOR

OR APPLICATION NUMBER: 60/080165

OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080194

OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080327

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080328

PRIOR PRIOR PRIOR PRIOR

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R FILING DATE: 1998-03 R APPLICATION NUMBER: R FILING DATE: 1998-03 R APPLICATION NUMBER:

1998-03-31

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FILING DATE: 1998-03-31

APPLICATION NUMBER: 60/ FILING DATE: 1998-03-30 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0

APPLICATION NUMBER:

PRIOR

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FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-01

60/080333

FILING DATE: 1998-0 APPLICATION NUMBER:

R FILING DATE: 1998-04-01
RR APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-08
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GENERAL INFORMATION:
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Best Local
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PRIOR
                                                         FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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APPLICANT:
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                                                                                                  APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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   PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Baker Kevin P
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                                                                                          REFERENCE: P2630P1C7
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-15
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                  Williams, P. Mickey
                                                                                                                                                                     Tumas, Daniel
                                                                                                                                                                                 Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen,
                                                                                                                                                                                                                                                                                                                                                                                                      Gerber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleon Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                        Goddard
                                                                                                                                                                                                                                    Paoni,
                                                                                                                                                                                                                                                             Napier, Mary A.
                                                                                                                                                                                                                                                                                               Kljavin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eaton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09978189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                          sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                   Wei-Qiang
                                                                                                                                                                                                                                                    James;
                                                                                                                                                                                                                                  Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-05-07
                                                                                                                                                                                                                                                                                                                                                                      , Audrey
                                                                                                                                                                                                                                                                                                                                                                                     Hanspeter
en, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.4%; 36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/085580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                          Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
OR FILING DATE: 1998-04-08

OR APPLICATION NUMBER: 60/081203

OR FILING DATE: 1998-04-09

OR APPLICATION NUMBER: 60/081229

OR FILING DATE: 1998-04-09

OR APPLICATION NUMBER: 60/081955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-27
                                                                                                                                                                  APPLICATION NUMBER: 60/
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/
FILING DATE: 1998-04-08
                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/
FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-20
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                                                                         APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
                                                                                                       APPLICATION NUMBER: FILING DATE: 1998-04
                                                                                                                                      APPLICATION NUMBER: 60/
FILING DATE: 1998-04-08
                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          FILING DATE: 1998-0 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/080327
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 1998-0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-0: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-03-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                         1998-04-08
                                                                                                                       60/081071
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                                                                                                                                                                                                                                               60/080333
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3-27
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                                                                                                                                                                                                                                                                            60/080328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60/079663
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DR APPLICATION NUMBER: 60/081819
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081952
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081838
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR APPLICATION NUMBER: 60/082569

APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15

FILING

DATE: 1998-04-15

FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804

60/082700

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APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

60/083392

APPLICATION NUMBER: 60/083495

FILING DATE: 1998-04-

APPLICATION NUMBER: 60/083322

FILING DATE: 1998-04-APPLICATION NUMBER: 60 FILING DATE: 1998-04

FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/

60/083545 60/083499 60/083496

APPLICATION NUMBER:

FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27

APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/082797 APPLICATION NUMBER: 6 FILING DATE: 1998-04-22

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RESULT 12
US-10-028-072-272
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                        PRIOR PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
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                                                                                                                                                                                                                          PRIOR
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR APPLICATION NUMBER: 60/085689
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
OR APPLICATION NUMBER: 60/059184
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059263
OR FILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/059352
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059588
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059686
OR FILING DATE: 1997-09-24
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                                                                                                                                                                                  APPLICATION NUMBER: 60/059117
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/059113
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059115
FILING DATE: 1997-09-17
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Similarity 36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beresini, Maureen
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5. US20030004311A1
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PRIOR PRIOR

FILING DATE: 1998-5-07 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/

60/084600 60/084598

OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13

PRIOR

FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/0 FILING DATE: 1998-05-06

60/084441

APPLICATION NUMBER: 60/0 FILING DATE: 1998-05-05

FILING DATE: 1998-04-30 APPLICATION NUMBER: FILING DATE:

APPLICATION NUMBER:

60/084414 60/084366 APPLICATION NUMBER: 60/

1998-04-29

60/083742 60/083500 APPLICATION NUMBER: FILING DATE:

1998-04-29 1998-04-29 1998-04-

60/083558

60/083559

APPLICATION NUMBER:

APPLICATION NUMBER: FILING DATE:

60/083554

PRIOR

PRIOR PRIOR

APPLICATION NUMBER: 60/ APPLICATION NUMBER:

60/084637

60/084639

APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR APPLICATION NUMBER: 60/063082
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31

OR APPLICATION NUMBER: 60/062250
OR FILLING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILLING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062287
OR FILLING DATE: 1997-10-17

PRIOR PRIOR

APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24

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PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
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OR APPLICATION NUMBER: 60/063755
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064809
OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/065186
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OR FILING DATE: 1997-11-24

OR APPLICATION NUMBER: 60/066770

OR FILING DATE: 1997-11-24

OR APPLICATION NUMBER: 60/069212

OR FILING DATE: 1997-12-11

OR APPLICATION NUMBER: 60/069278

OR FILING DATE: 1997-12-11

OR APPLICATION NUMBER: 60/069334

OR FILING DATE: 1997-12-11

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OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-04

PRIOR PRIOR

OR APPLICATION NUMBER: 60/074086
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OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR APPLICATION NUMBER: 60/079294
OR APPLICATION NUMBER: 60/079663

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CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 272
LENGTH: 323
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-272
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US-10-123-904-272
Sequence 272, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
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                               APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
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13; Conservative
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
              Desnoyers, Luc
Filvaroff, Ellen
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 Gao, Wei-Qiang
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9; Mismatches
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LENGTH: 323
TYPE: PRT
ORGANISM: Homo Sapien
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NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2002-04-16
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CURRENT FILING DATE: 2002-05-06
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Godowski, Paul J.
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TGWIV---LVVSVILL-----GVASHIDNYQPPEQ 34

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Search completed: February $\,$ 6, 2003, 21:40:11 $\,$ Job time : 12 $\,$ secs

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SUMMARIES

Result No. 0 0 000 469 449.8 449.8 347 347 30.6 106.6 103.4 42.4 42.4 42.4 42.2 41.8 41.8 41.8 41.9 41.0 41.0 41.0 41.0 41.0 100.0 10 Query Match 180854 197092 6294 9997 189295 189295 18446 19132 157672 178493 11321 11541 74589 12668 58753 164051 145938 19211 23009 233050 134978 164184 167577 190015 67890 175111 204591 204591 169824 173770 106859 7448 13259 257071 358 Length DΒ AB026660 ATH131517 AC100742 AL354981 AE006407 AE0079445 AF079445 AF1079445 AF10889 AC1188165 AC10796 AC036155 AC344308 AX344308 AX345270 AC113717 AC012568 AB007651 AC113717 AC012568 AB007650 AC013716 D90805 AE008763 AL627271 AC079004 AC079004 AC099687 AL591126 AC101999 AC122262 AC1122262 AC01089118 AC122716 AC069118 AC122716 AC010295 AC010295 AC010295 H ALIGNMENTS D90805 E. coli geno AE008763 Salmonell AL627271 Salmonell AC079004 Homo sapi AC079006 Homo sapi AC079068 Homo sapi AC079068 Homo sapi AC079068 Homo sapi AC079070 Mus muscu AC101099 Mus muscu AC122262 Mus muscu AC010876 Homo sapi AC022716 Homo sapi AC022716 Homo sapi AC022716 Homo sapi AC022716 Homo sapi AC010295 Homo sapi AC010295 Homo sapi AC010295 Homo sapi AC010295 Homo sapi AC010395 Homo sapi AF05305 Dictyoste AB0101068 Arabidops AC1007813 Clostridi AB010068 Arabidops AF079445 Dictyoste AF079445 Dictyoste AF079445 Caenorhab AX278241 Sequence AE000258 Escherich D90806 E.coli geno D90807 E.coli geno D90807 E.coli geno AE005386 Escherich AP002558 Escherich AF219227 Escherich AE007813 AB010068 AF079445 AF125459 AC1128165 AC128165 AC474377 AC107960 AC036155 AX344308 AX281373 Description Homo sapi Rattus no Dictyoste Homo sapi Homo sapi Sequence Sequence Sequence Rattus no Mus mus mus Rattus no

JOURNAL	TITLE	AUTHORS	REFERENCE	-		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX278241	RESULT 1
Patent: WO 0177176-A 1 18-OCT-2001;	Novel blr molecules affecting antibiotic susceptibility	Levy, S.B. and Mcmurry, L.M.	1	Escherichia.	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	Escherichia coli	Escherichia coli.		AX278241.1 GI:16605287	AX278241	1 from Patent W	AX278241 481 bp DNA linear PAT 01-NOV-2001		

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Blattner, F.R., Plunkétt, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Escherichia coli K12
Bacteria; Proteobacteria; gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA, Wisconsin, 445 Henry Mall, Madison, WI 53706, USA, On Sep 9, 1997 this sequence version replaced gi:1787907.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, Kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG site Nos., unique ID nos. for the genes in the E. coli Genetic (http://cgsc.biology,yale.edu). Annotation of the database is accessible (http://cgsc.biology,yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated updated information will be available at the E. coli cenome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica and products; all new functional assignments courtesy of Monica heginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 13172)
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                                                                                                                                                                                              /gene="malx"
/gene="malx"
/function="transport; Transport of small molecules:
/function="transport; Transport of small molecules:
/function="transport; Transport of small molecules:
/function="color: Transport of small mol
     /product-"pTS system, maltose and glucose-specific II ABC" (protein id-"AAC74693.1" /dp.xref-"GI:787908" /translation-"MTAKTAPKVTLWEFFQQLGKTFMLPVALLSFCGIMLGIGSSLSS HDVITLIPVLGNPVLQAIFTWMSKIGSFAFSFLPVMFCIAIPLGLARENKGVAAFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /note="b1621"
76. .1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sub_strain="MG1655"
/db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="malX"
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                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/product="enzyme that may degrade or block biosynthesis endogenous mal inducer, probably aminotrasferase"
/protein_id="AAC74694.1"
/db_xref="GI:1787909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGYAVMILAVNFWLTNKGILPTTDAAVLKANNIQSILGIQSIDTGILGAVIAGIIVWM
LHERFHNIRLDALAFFGGTRETVEISLUMGLVGLIVL PLWWPLFAMGLSGLGHNINS
AGDEGEMLFGTGGERLLLPFGLHHILVALIRFTDAGGTQEVCAGTVSGALTIFQAQLSC
PTTHGFSESATRFLSQGKMPAFLGGLPGAALAMYHCARPENRHKIKGLLISGLIACVV
GGTTEBLFLFLFAPVLYVLTFAFATTRFNLKTPGBOSETVASVLGVIIGNIDFVVFGILHG
LSTKRYMYMPVAAIWFVYLYVIFAFATTRFNLKTPGBOSETVASVLASSIEKAVAGAPCKSGY
LSTKRYMYMPVAAIWFVLYVIFAFATTRFNLKTPGBOSETVASVLGVASIEKAVAGAPCKSGY
LSTKRYMYMPVAAIWFVLYVIFAFATTRFNLKTPGBOSETVASVLGVAGHULQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="
2954...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MFDFSKVVDRHGTWCTQWDYVADRFGTADLLPFTISDMDFATAP
CIIEALNQRLMHGYFGYSRWRNDEFLAAIAHWFSTOHYTAIDSGVVVVGPSVIYMVSE
LIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLAK
PECKIMLLCSFQNPTGKVWTCDELEIWADLCERHGYRVISDEHMDMWWGEQPHIPWS
NVARGDWALLTSGSKSFNIFALTGAYGIIENSSSRDAYLSALKGRDGLSSPSVLALTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              င္ပ
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/translation="mSNSHHTSMRGNDMSDNIRVGLIGYGYASKTFHAPLIAGTPGQE
LAVISSSDETKVKADWPTVTVVSEPKHLFNDPNIDLIVIPTPNDTHFPLAKAALEAGK
HVVVDKPFTVTLSQARELDALAKSLGRVLSVFHNRRWDSDFLTLKGLLAEGVLGEVAY
                                                                                         /product="orf, hypothetical protein"
/protein_id="AAC74696.1"
/db_xref="GI:1787911"
                                                                                                                                                                                                                                                                   /note="f359; residues 74-259 are 45 pct identical
aa62-244 from hypothetical protein YHHX_ECOLI SW:
                                                                                                                                                                                                                                                                                                                                                                                           complement(3989. .5068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDDPGVQGVDIIHEYTVAAPAAGLSREQIRQAQINGLEMAFLSAEEKRALREKVAAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMAMAHQLPVAGVVEAVIDGVREGCRTFGVQAKLIGIMSRTFGEAACQQELEAFLAHR
DQITALDLAGDELGFPGSLFLSHFNRARDAGWHITVHAGEAAGPESIWQAIRELGAER
IGHGVKAIEDRALMDFLAEQQIGIESCLTSNIQTSTVAELAAHPLKTFLEHGIRASIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHVQVIANEPDLVSFLTKLDWGVKVLASLDACRRVAFENIEDAARHGLHYVELRFSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="adenosine deaminase"
/protein_id="AAC74695.1"
/db_xref="GI:1787910"
/translation="MIDTTLPLTDIHRHLDGNIRPQTILELGROYNISLPAQSLETLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SW: P22333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="enzyme; Salvage of nucleosides and nucleotides"
/note="0333; This 333 aa ORF is 99 pct identical (1 gap)
to333_residues 332 aa protein ADD_ECOLI; CG Site No. 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNID
DNALOKALIEQEKVAIMPGYTYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /noie="0390; 100 pct identical to MALY_ECOLI SW: CG Site No. 32257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1678. .2850
/gene="maly"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="b1624"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="factor Sigma54;
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                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                function="orf; Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5068
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Best Local
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                                                                                                                                                                                                                                                                                                                            1 TGCCTCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTT
                                                                                                                                                                                                                                                                   CAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT
GATATTAAACCAGGAATTTATTATCTTGTTCGATGTTGTTGGTGATTGTCAGGGATAGTA 480
                                          GTAAGCTCTGCACTTGTGGAGCGACATGCTGCCCGTCCGGGTGCATGTTTTCACTTGTCG
                                                                               CAACG-ACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT
                                                                                                                                                                                                                                                                                                                                                                    TGCCTCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTT
                           GTAAGCTCTGCACTTGTGGAGCGACATGCTGCCCGTCCGGGTGCATGTTTTCACTTGTCG
                                                                                                                                                                    GAATCGTCTTATTGAATTAACAGGTTGGATCGTTCTTGTCGTTCAGTCATTCTTCG
                                                                                                                                                                                                                          AATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTC
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/note="factor Sigma70; predicted +1 start 5670. .5885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="factor Sigma70; 5947. .6411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="REP (repetitive extragenic
contains 1 REP sequence"
complement(5165...5193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf; Unknown"
/note="071; This 71 aa ORF
to71 residues of an approx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAIQVMELIELGIESAKHRATLCLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FESHFDRFRPQVRDRWREQGGPGSGIWYDLAPHLLDQAITLFGLPVSMTVDLAQLRPG
AQSTDYFHAILSYPQRRVILHGTMLAAAESARYIVHGSRGSYVKYGLDPQEERLKNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTVQDYLLKFRKISSLESLEKLYDHLNYTLTDDQELINMYRAAD
HRRAELVSGGRLFDLGQVPKSVWHYVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="orf, hypothetical
/protein_id="AAC74697.1"
/db_xref="GI:1787912"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="o154; This 154 aa ORF is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="b1626"
/function="orf; Unknown"
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/gene="b1625"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="factor Sigma70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="b1
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/gene="b1625"
                                                                                                                                                                                                                                                                                                                                                                                                                                       97.5%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor Sigma70; predicted +1 start at 1702836"
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 469;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sigma70;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted +1 start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted +1 start at 1702461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted +1 start
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       .5e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 pct identical
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DEFINITION
ACCESSION
VERSION
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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D90806.1 GI:1742679
Complete and shotgun sequencing; add; hdhA, hsdH; malI; malX; malY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group:
The Japan E.coli genome DNA sequencing group
Members: (1995.4 - 1996.3)
Alba,H. Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
Horluchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N.,
Sampel,G., Saki,Y., Tagami,H., Takemoto,K., Wada,C.,
Yamamoto,Y. and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-DEC-1996) Hirotada Mori, and Technology, Res. & Edu. Center for Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aibà, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inadd, T., Isono, K., Isono, S., Itch, T., Kanai, K., Kasai, H., Kashimoto, K., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishino, Y., Oshima, T., Motomura, K., Nakamura, Y., Nashimoto, H., Nishino, Y., Oshima, T., Rotto, N., Rashimoto, H., Nishino, Y., Oshima, T., Mizobuchi, R., Nakamura, Y., Nashimoto, H., Nishino, Y., Oshima, T., Motomura, Y., Nashimoto, H., Nishino, Y., Oshima, T., Motomura, Y., Nashimoto, H., Nishino, Y., Oshima, T., Mashimoto, H., Nishino, Y., Oshima, T., Mizobuchi, M., Nishino, Y., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660, Fax:81-7437-2-5669)
Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The systematic sequencing of the Escherichia coli genome in Japan Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salto,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library clone:Kohara clone #315
                                                                                                                                                                                                                                                                                                                           URL:
The Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mori, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Information operator:
Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Address: National Institute E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Japan E.coli genome DNA sequencing project
                                                                                                                                                                                                                                                                                       http:bsw3.aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                            E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 15332)
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/clone="Kohara clone #315"
/clone_lib="Kohara lambda miniset library"
                                                                                                                                             /organism="Escherichia
/strain="K12"
                                                                            /map="36.6 min"
                                                                                                         /db_xref="taxon:562"
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           E. coli genome database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                 coli"
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Genetic Info.; 8916-5
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2351. .3943
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                                                  /gene="malY"
3953. .5125
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/transl_table=11
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complement(269. .1036)
/gene="hdhA, hsdH"
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complement(<1. .48)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2351. .3943
/gene="malX"
/note="ORE_ID:0314#7
similar to [PIR Accession Number B42477]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="matakkitihdvalaagvsvstvslvlsgkgristatgervnaa
IEELGFVRNRQASALRGGQSGVIGLIVRDLSAPFYAELTAGLTEALEAQGRMVFLLHG
GKDGEQLAQRFSLLLNQGVDGVVIAGAAGSSDDLRRMAEEKAIVIFASRASYLDDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:0314#6 similar to [SwissProt Accession Number P18811]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1148. .2176)
/gene="mall"
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SSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTDALKSVITPEIEQKMLQHTPIRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Potential acrAB
/protein_id="BAA15376.1"
/db_xref="GI:1742680"
                                                        GGTTEPLEFLFLAFVLYVIHALLTGLGFTVMSVLGVTIGNTDGNIIDFVVFGILHG
LSTKWYMVPVVAAIWFVVYYVIFRFAITRFNLKTPGRDSEVASSIEKAVAGAPGKSGY
NVPAILEALGGADNIVSLDNCITRLRLSVKDMSLVNVQALKDNRAIGVVQLNQHNLOV
                                                                                                                                                 /translation="MTAKTAPKVTLWEEFFQQLGKTFMLPVALLSFCGIMLGIGSSLSS
HDVITLIPVLGNPVLQAIFTMMSKIGSFAFSFLPVMFCIAIPLGARENKGVAAFAGF
HDVITLIPVLGNPVLQAIFTMMSKIGSFAFSFLPVMFCIAIPLGALARENKGVAAFAGF
LGYAVMALAVAFFMLTNKGILFTDAAVLKANNIQSILGIQSIDGILGAVLAGIIVWM
LHERCHNIRLDALAFFGGTBRVPIISSLVMCLVGLVIPLVWPIFAMGISGLGHMINS
AGDFGPMLFGTGERLLLPFGLHHILVALIRFTDAGGTQEVCGQTVSGALTIFQAQLSC
PTTHGFSESATRFLSQCKMPAFLGGLPGAALAMYHCARPENRHKIKGLLISGLIACVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVRPDNMQAAQLLTEHLIRNGHQRIAWLGGQSSSLTRAERVGGYCATLLKFGLPFHSD
WVLECTSSQKQAAEAITALLRHNPTISAVVCINETIAMGAWFGLLKAGRQSGESGVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Maltose regulon regulatory protein MalI."
/protein_id="BAA15378.1"
/db_xref="GI:1742682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1148. .2176)
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adaanhvvdelqolggqafacrcbitseqelsaladealsklgkvbilvnnaggggpk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="7-a-hydroxysteroid dehydrogenase (EC
(7-alpha-HSDH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to [SwissProt Accession Number P25529]"
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/gene="hdhA, hsdH"
/note="ORF_ID:0314#5
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                                                                                                                                                                                                                                                                                                                                                                                                            /product="Phosphotransferase
2.7.1.69) Malx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA15377.1"
/db_xref="GI:1742681"
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VIGPQVQSVKDEMAGLMHTVQA"
3953. .5125
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                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA15379.1"
/db_xref="GI:1742683"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"Ferredoxin II."
/protein_id="BAA15383.1"
/db_xref="G:1742687"
/db_xref="G:1742687"
/db_xref="G:1742687"
/cb_xref="G:1742687"
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/protein_id="BAA15382.1"
/protein_id="BAA15382.1"
/db_xref="Gi:1742686"
/translation="msnshhtsmrgndmsdnirvgligygyasktfhapliagtpgge
/translation="msnshhtsmrgndmsdnirvgligtprnthfplakaaleagk
LAVISSSDETKVKADMPTVTVYSEPKHLFNDPNIDLIVITFTRNTHFPLAKAALEAGK
HVVVDKPFTVTLSQARELDALAKSLGRVLSVFHNRRMDSTTLKGLLABGVLGEVAY
FESHFDRFRPGVRDRWEEGGEPGSGIWYDLAPHLLDQAITLFGLPVSMTVDLAQLRFG
FORDYFHAILSYPORRVILHGTMLAAAESARYIVHGSRGSYVKYGLDPQEERLKNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF_ID:0316#5
similar to [SwissProt
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/db_xref="GI:1742685"
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/translation="MFDFSKVVDRHGTWCTQWDYVADREGTADLLPFTISDMDFATAP
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Direct Submission
Direct Submission
Submitted (14-DEC-1996) Hirotada Mori, NAKA IIISLELLE,
Submitted (14-DEC-1996) Hirotada Mori, Organization of Submitted (14-DEC-1996) Hirotada Mori, Organization of Submission 
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97251357
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E.coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto,Y. and Horiuchi,T.
A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage r DNA Res. 3 (6), 363-377 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aiba, H., Baba, T., Fujita, K., Hayashi, K., Inada, T., Isono, K., Itoh, T., Kasai, H., Kashimoto, K., Kimura, S., Kitakawa, M., Kitagawa, M., Makino, K., Miki, T., Mizobuchi, K., Mori, H., Mori, T., Motomura, K., Nakade, S., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Sivasundaram, S., Tagami, H., Takeda, J., Takemoto, K., Takeuchi, Y., Wada, C.,
                                                                                                                                                                                                                            Yamamoto, Y. and Yano, M. The systematic sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli (strain:K12) DNA, library clone:Kohara clone #317.
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D90808.1 GI:1742711
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                                                                                                                                                                      (bases 1 to 15601)
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                                                                            NARA Institute of Science
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Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Members: (1995.4 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikoma, 630-01, Japan
E-mail: hmori@gtc.aist-nara.ac.jp
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Address: NARA Institute of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Address: National Institute E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Japan E.coli genome DNA sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(<1. .149)
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/clone=lib="Kohara lambda miniset library"
/clone="Nucleotide position 1699735-1715335 from the
initiation site of ThrA (0 min.).~This clone is from
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                                                                        complement(1249. .2277)
                                                                                                                         complement(1249.
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(7-alpha-HSDH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="hdhA, hsdH"
/note="nor";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Potential acrAB operon /protein_id="BAA15406.1" /db_xref="GI:1742712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="K12"
               /note="ORF_ID:0314#6
                                                                                                                                                                                                                                                                    /protein_id="BAA15407.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="hdhA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"taxon:562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation-"MMDNMQTEAQPTRTRILNAAREIFSENGFHSASMKAICKSCAIS
                                                   /gene="mali"
                                                                                                                                                                                                                                                                                                                                                                                              codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nara 630-01, Japan
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. hsdH"
[SwissProt Accession Number P18811]"
                                                                                                                         . 2277)
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GKDGEGLAQRRSLLLMQGVDGVVIAGAAGSSDDLRRWAEEKALFVIFASRASYLDDVD
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AGDFGPMLFGTGERLLLPFGLHHILVALIRFTDAGFGEVCGGYVSGALTIFQAQLSC
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5330. .6331
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HIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNID
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4054. .5226
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2.7.1.69) MalX"
/protein_id="BAAL5409.1"
/db_xref="GI:1742715"
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/gene="malx"
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                                                                 IGHGVKAIEDRALMDFLAEQQIGIESCLTSNIQTSTVAELAAHPLKTFLEHGIRASIN
TDDPGVQGVDIIHEYTVAAPAAGLSREQIRQAQINGLEMAFLSAEEKRALREKVAAK"
                                                                                                                                                                                                                                                                                                                                                      aminohydrolase)."
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                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                   /product="Adenosine deaminase (EC 3.5.4.4) (Adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                        .7444)
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gene

CDS

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to [SwissProt Accession Number P37168]"

gene CDS

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REFERENCE
                                                                                                                     SOURCE
                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                             VERSION
                                                                                                                                                                                               ACCESSION
                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GTAAGCTCTGCACTTGTGGAGCGACATGCTGCCCGTCCGGGTGCATGTTTTCACTTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CAACGAACAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT
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                                                                                                                                                                                                                                                                                                                                                                                                         GATATTAAACCAGGAATTTATTATCTTGTTCGATGTTGTTGGTGATTGTCAGGGATAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAAGCTCTGCACTTGTGGAGCGACATGCTGCCCGTCCGGGTGCATGTTTTCACTTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATCGTCTTATTGAATTAACAGGTTGGATCGTTCTTGTCGTTTCAGTCATTCTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGGCGAGTCACATTGACAACTATCAGCCACCTGAACAGAGTGCTTCGGTACAACACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480;
                                                                                                                                                     E.coli genomic DNA, Kohara clone #316(
D90807 AB001340
D90807.1 GI:1742692
Complete and shotgun sequencing; add;
                                                                        Escherichia coli
                                        Escherichia.
                                                            Bacteria;
                                                                                                               Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda miniset
                                                                                                                                                                                                                                      D90807
                                                                                                library clone:Kohara clone #316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
Baba,T.,
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AQSTDYFHAILSYPQRRVILHGTMLAAAESARYIVHGSRGSYVKYGLDPQEERLKNGE
RLPQEDWGYDMRDGVLTRVEGEERVEETLLTVPGNYPAYYAAIRDALNGDGENPVPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to [SwissProt Accession Number P00211]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAIQVMELIELGIESAKHRATLCLA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSNSHHTSMRGNDMSDNIRVGLIGYGYASKTFHAPLIAGTPGQE
LAVISSSDETKVKADWPTVTVVSEPKHLFNDPNIDLIVIPTPNDTHFPLAKAALEAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA15412.1"
/db_xref="GI:1742718"
                                                          Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Virulence
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Fujita, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 469; DB 1;
Pred. No. 2.4e-112;
0; Mismatches 0;
                                                                                                                                                                                                              20231 bp DNA linear BC ara clone #316(36.7-37.1 min.).
                                                      gamma
Hayashi,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor Mvim."
                                                        subdivision;
                                                                                                                                                     gst; nth; pdxH; tyrS; ydhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15601;
Inada, T.,
                                                        Enterobacteriaceae;
                                                                                                                                                                                                                                  BCT 29-MAY-1997
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JOURNAL
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MEDLINE
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Submitted (14-DEC-1996) Hirotada Mori,
and Technology, Res. & Edu. Center for
Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashinoto, K., Kin, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Kitakawa, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh, T., Kasai, H., Kashimoto, K., Kimura, S., Kitakawa, M., Kitaqawa, M., Makino, K., Miki, T., Mizobuchi, K., Mori, H., Mori, Motomura, K., Nakade, S., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Sivasundaram, S., Tagami, H., Takeda, J., Takemoto, K., Takeuchi, Y., Wada, C., Yamamoto, Y., and Horiuchi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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97251357
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Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660
Fax:81-7437-2-5669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The systematic sequencing of the Escherichia coli genome in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Headed by:
Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kin,S., Kinura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Makamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamammoto,Y., and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Address: National Institute E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Japan E.coli genome DNA sequencing group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Address: NARA Institute of Science Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http:bsw3.aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Japan E. coli genome database
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                                                                                                                                                                                                                             /clone="Kohara clone #316"
/clone=1b="Kohara lambda miniset library"
/clone_lib="Kohara lambda miniset library"
/note="Nucleoride position 1705226-1725456 from the
initiation site of Thra (0 min.).-This clone is from
                              similar to [SwissProt
                                                                                                                                                                                                     Kohara lambda miniset library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
/codon_start=1
                                                         /note="ORF_ID:o314#9
                                                                                 /gene="add"
                                                                                                                                           /gene="add"
                                                                                                                                                                                                                                                                                                                                                         /map="36.7 min"
                                                                                                                                                                                                                                                                                                                                                                                                          /strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:562"
                                                                                                                   .840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute of Basic Biology, Okazaki, 444, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Japan
                              Accession Number P22333] "
                                                                                                                                                                                                                                                                                                                                                                                                                                        coli"
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Genetic Info.; 8916-5
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CDS

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/ LTAINSI ALLON- MIKKLESAFRKNKIMDENGGIHPPEMKIQSNGTPLROVPLAORFV
/ LTAINSI ALLON- MIKKLESAFRKNKIMDENGGIHPPEMKIQSNGTPLROVPLAORFV
| IPLKQHIGAEGELCVSVGDKYLRGQDLTRGROKMLPVLAPTSGTVTA LAPHSTAHPSA
| LAELSYIIDADGEDCWIPRDGWAD/KRRSKEELIERIHQEGVAGLGGAGFPTGVKLQG
| GDK TETLIINAASCEPYITADDRLMQDCAAQVVEGIRILAHLLQPREILIGIEDNKP
| QAISMLRAVLADSNDISLRVIPTKYPSGGAKQLTYILTGKQVPHGGRSSDIGVLMONV
| GTAYANVRAVIDGEPTTERVVTLTGEA LARFGNVWARLGTPVRHILLNDAGFCPSADQM
| VIMGGPLMGFTLPWLDVPVKITNCLLAPSANELEBQEGSCIRCSACADGCPADLL
| PQQLYMFSKGQQHDKATTHNIADCIECGACAWVCPSNITLVQYFRQEKAEIAAIRQEE
| KRAABEAKARFEBRQANEREKAARLERHKSAAVQPAAKDAIAALARFVKEKQAQAT
| QPIVIKAGERPDNSAIIAARERRKAVEAAIARAKARKLEQQQANAEPEEQVDPRKAAVE
| AAIARAKARKLEQQQANAEPEQQVDPRKAAVEAAIARAKARKLEQQPANAEPEEQVDP
| ARAKARKLEQQQANAEPEQQVDPRKAAVEAAIARAKARKLEQQPANAEPEEQVDP
| RKAAVEAAIARAKARKLEQQQANAVPEEQVDPRKAAVAAAIARARARKARQAKKAAQQKVVNED
| RKAAVEAAIARAKARKLEQQQANAVPEEQVDPRKAAVAAAIARARARKARQAKKAAQQKVVNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Ferredoxin II."
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/db_xref="GI:1742695"
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ITPARMYAVIDENNCIGCTKCIQACPVDAIVGATRAMHTVMSDLCTGCNLCVDPCPTH
CISLQFVAETFDSWKWDLNTIFVRIIFVEHHA"
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FESHFDRFRPQVRDRWREDGGEGGIWYDLAPHLDQAITLFGLPYSMTVDLAQLRGE
ALPGEBMGYDMRDGVLTRVEGGERVEBTLLFUPGNYPAYYAAIRDALNGDGENPVPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSPGYMAMAHOLPVAGVVEAVIDGVREGCRTFGVQAKLIGIMSRTFGEAACQQELEAF
LAHRDQITALDLAGDELGFPGSLFLSHFNRARDAGWHITVHAGEAAGPESIWQAIREL
GAERIGHGVKAIEDRALMDFLAEQQIGIESCLTSNIQTSTVAELAAHPLKTFLEHGIR
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similar to [SwissProt Accession Number P00211]"
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3954. .4532
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AIQLLVGADFNGTVLGTRVTEHHETPGLGDKIELRLSDWITHFAGKKISGADDAHWAV
                                                                                                                                                                                                                                                                                                               /note="ORF_ID:o316#10
similar to [SwissProt Accession Number P44291]"
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/transl_table=11
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                                                                                         KKDGGDFDQFTGATITPRAVVNAVKRAGLYAQTLPAQLSQLPACGE"
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/note="ORF_ID:o316#11
similar to [SwissProt Accession Number P43959]"
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                CGTGGCGAGTCACATTGACAACTATCAGCCACCTGAACAGAGTGCTTCGGTACAACACAA
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1980 AATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTC
                                     CAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT 180
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9129. .9764
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'gene-"nth'

'note-"ORT_ID:0316#12

'note-"ORT_ID:0316#12

Similar to [PIR Accession Number A32412]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Traislation="morpanokrytesyslnafkopkafyllifsielwerfgyyglogim
AVYLVKOLGMSEADSITLFSSESALYYGLVAIGGWLGDKVLGTKRVLMLGAYVLAIGY
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IGSFESMIATPWLAAKYGMSVAFALSVYGLLTIVNEAFCORWYKQYGSKPDEEPINY
RNLLLTIIGVVALIAIATWLLHNQEVARMALGVVAFGIVVIFGKEAFAMKGAARRKMI
VAFILMLEAIIFFYLYSOMPTSLNFFAIRNVEHSILGLAVEPEQYQALNPFWIIIGSP
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vsvnkartakvltpantsakvlentakvetriktiglinskaenitkterilleohng
evpedraalbalegverktaavvlurtaargwptiavdthiervonttgrapgknveqve
ekllkvvpaefkvdchhwlilhgrytciarkprogsciiedlceykekvdi"
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similar to [SwissProt Accession
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3.1.25.1)"
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/db_xref="GI:1742699"
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2339
                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATATTAAACCAGGAATTTATTATTATCTTGTTCGATGTTGTTGGTGATTGTCAGGGATAGTA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A 2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATATTAAACCAGGAATTTATTATCTTGTTCGATGTTGTTGGTGATTGTCAGGGATAGTA 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Bohan, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of enterohaemorrhagic Nature 409 (6819), 529-533 (2001) 21074935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A., Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L., Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K., Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE005386 AE005174
AE005386.1 GI:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-OCT-2000) Laboratory of Genetics, Wisconsin, 445 Henry Mall, Madison, WI 53706, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE005386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 13259)
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                                                                                                                                                                                                                                                                             /function="transport; Transport of small molecules:
Carbohydrates, organic acids, alcohols"
/note="Residues 1 to 530 of 530 are 99.43 pct identical to
residues 1 to 530 of 530 from Escherichia coli K-12 Strain
               /translation="MTAKTAPKVTLWEEFFQQLGKTFMLPVALLSFCGIMLGIGSSLSS HDVITLLPVLGNPVLQAIF"MMSKIGSFAFSFLPVMFCIAIPLGLARENKGVAAFAGF VGYAVMNLAVNFWLTNKGILPTTDAAVLKANNIQSILGIQSIDTGILGAVIAGIIVMM LHERRHNIRLJBALAFFGGTPRFVPIISSLVMGLVGLVIPLVMPIFAMGISGLGHMINS AGDFGPMLFGTGERLLLPFGLHHILVALIRFTDAGGTQEVCGQTVSGALTIFQAQLSC PTTHGFSESATRFLSQGKMPAFLGGLPGAALAMYHCARPENRHKIKGLLISGLIACVV
GGTTEPLEFLFLFVAPVLYVIHALLTGLGFTVMSVLGVTIGNTDGNIIDFVVFGILHG
                                                                                                                                                /product="PTS system, maltose and
/protein_id="AAG56610.1"
/db_xref="GI:12515610"
                                                                                                                                                                                                                                                             MG1655: B1621"
                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                              'note="22626"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="malx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Escherichia coli 0157:H7
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                         /gene="malx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .13259
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EDL933
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ntig 3 of
                                                                                                                                                                                           glucose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDL933"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glasner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 21-MAR-2001
3, section 5 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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/gene="add"
/note="22628"
2996. .3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4033..5112)
/gene="z2629"
complement(4033..5112)
/gene="z2629"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="enzyme that may degrade or block biosynthesis of endogenous mal inducer, probably aminotrasferase" /protein_id="AAG56611.1" /db_xref="G::12515611" /translation="MFDFSKVVDRHGTWCTQWDYVADRFGTADLLPFTISDMDFATAP
                                                                                                                        /gene="Z2631"
5715. .5930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="enzyme: Central intermediary metabolism: Salvage of nucleosides and nucleotides"
/note="Residues 1 to 33 of 33 are 99.39 pot ident residues 1 to 33 of 33 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVARGDWALLTSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGLSSPSVLALTA
HIAAYQQGAPWLDALRVYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNID
DNALQKALIEQEKVAIMPGYTYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR"
                                                                                                                                                                                        RLPQEDWGYDMRDGVLTRVEGEERVEETLLTVPGNYPAYYAAIRDALNGDGENPVPAS
QAIQVMELIELGIESAKHRATLCLA"
5715. .5930
                                                                                                                                                                                                                                                                                ĹAVISSSDETKVKADWPTVTVVSEPKHLFNDPNIDLIVIPTPNDTHFPLAKAALEAGK
HVVVDKPFTVTLSQAKELDALAKSLGRVLSVFHNRRWDSDFILLAEGVLGEVAY
FESHEDDRFRPQVRDKWREDGGPGSGTWYDLAPHLDDA,ITLFGLPVSMYDULAQLRP
AQSTDYFHAILSYPQRRVILHGTMLAAAESARYIVHGSRGSYVKYGLDPQEERLKNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MG1655: B1624"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf; Unknown function"
/note="Residues 1 to 359 of 359 are 99.72 pct identical to residues 1 to 359 of 359 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MIDTTLPLTDIHRHLDGNIRPQTILELGRQYNISLPAQSLETLI
PHYQVIANEPDLYSFLTKLDWGVKVLASLDACRRVAFENIEDAARNGLHYVELRFSPG
YMAWAHQLPVAGVVEAVIDGVREGCRTFGVQAKLIGIWSRTFGEAACQQELEAFLAHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="adenosine de
/protein_id="AAG56612.
/db_xref="GI:12515612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIIEALNQRLMHGVFGYSRWKNDEFLAAIAHWFSTQHYTAIDPQSVVYGPSVIYMVSE
LIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compounds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVPATLEALGGADNIVSLDNGITRLRLSVKDMSLVNVQALKDNRAIGVVQLNQHNLQV
VIGPQVQSVKDEMAGLMHTVQA"
1720. 2892
/function="orf; Unknown function"
/note="Residues 1 to 71 of 71 are 100.00 pct
residues 1 to 71 of 71 from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDDPGVQGVDIIHEYTVAAPAAGLSREQIRQAQINGLEMAFLNAEEKRALREKVAAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQITALDLAGDELGFPGSLFLSHFNRARDAGWHITVHAGEAAGPESIWQAIRELGAER
IGHGVKAIEDRALMDFLAEQQIGIESCLTSNIQTSTVAELAAHPLKTFLEHGIRASIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MG1655: B1623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="add"
/function="enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/product="enzyme that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MG1655: B1622"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG56613.
/db_xref="GI:12515613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="orf, hypothetical protein"
/nrotein id="AAG56613.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2996. .3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PECKIMLLCSPQNPTGKVWTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="maly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="maly"
                                                                                          /gene="Z2631"
                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSNSHHTSMRGNDMSDNIRVGLIGYGYASKTFHAPLIAGTPGLE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Residues 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme; Degradation of small molecules: Carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="22627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 390 of 390 are 99.23 pct identical to of 390 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deaminase"
12.1"
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identical to K-12 Strain

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gene
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                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                CDS
                                               Local Similarity
nes 463; Conserv
             TGCCTCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTT
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5992. .6456
/gene="z2632"
/function="orf; Unknown function"
/note="Residues 1 to 154 of 154 are 98.70
residues 1 to 154 of 154 from Escherichia
MG1655: B1626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Z263;
7114. .7692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Z2633"
6533. .7114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="orf, hypothetical protein"
/protein_1d="AAG56616.1"
/db_xref="GI:12515616"
/translation="wmpytllfvgTvLvnnFvLvKFLGLCPFMGVSKKLETAMGMGLA
/translation="wmpytllfvgTvLvlxTLAFILVIAVVVQFTEMVVRKTSFVLYRL
IGIFLPLITTNCAVLGVALLNINLGHHFLQSALYGFSAAVGFSLVMVLFAAIRERLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6533
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ALSSPQTFQTIGAQALTTQIIMGVSFITAIAMMYYTLWLTIAFFKRRCVPKHYIIWL
LISVLLAVKAFAFSPVEDGIAVRQULETLLATALIVFYFKRSSRVKATFVNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/transl_table=11
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/protein_id="AAQ56615.1"
/db_xref="GI:12515615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mtvQDYLLKFRKISSLESLEKLYDHLNYTLTDDQELINMYRAAD
HRRAELVSGGRLFDLGQVPKSVWHYVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="orf, hypothetical protein"
/protein_id="AAG56614.1"
/db_xref="GI:12515614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG1655: B1625"
                                                                                                                                                                                                                                            /translation="MNAIWIAVAAVXLLGLAFGAILGYASRREAVEDDPVVEKIDEIL
POSOCOGCGY VGCRPYABAISONGEKINRCAFGEAVKLKIAELLNVEPQPLDGEAQE
LTPARAWAN IDENNCIGCTKCIQACFVDAIVGATRAMHTVMSDLCTGCNLCVDPCPTH
LTPARAWAN IDENNCIGCTKCIQACFVDAIVGATRAMHTVMSDLCTGCNLCVDPCPTH
CISLQPVAETPDSWKWDLNTIPVRIIPVEHHA"
                                                                                                                                                                                                                                                                                                                                                                                                         /function="orf; Unknown function"
/note="Residues 1 to 192 of 192 are 98.95 pct identical to residues 1 to 192 of 192 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADVPAPFRGNAIALITAGLMSLAFMGFXGLVKL"
7114. .7692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_
                                                                                                                /function="putative membrane; Not classified"
/note="Residues 1 to 740 of 740 are 97.83 pct identical to
residues 1 to 740 of 740 from Escherichia coli K-12 Strain
MG1655: B1629"
                                                                                                                                                                             7685. .9907
/gene="Z2636"
                                                                                                                                                                                                                                                                                                             /transi_table=11
/transi_table=11
/product="orf, hypothetical protein"
/protein_id="Aw556617.1"
/db_xref="GI:12515617"
                                                                                                                                                                                                                                                                                                                                                                                             MG1655: B1628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Z2634"
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                                                                  Score 452.2; DB 1;
Pred. No. 6.2e-108;
                                                   Mismatches
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      Complete nucleotide sequence of the prophage VT1-Sakai carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia coli
                                        Shinagawa, H.
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Escherichia coli O157:H7 DNA, cc
AP002558 BA000007
AP002558.1 GI:13361764
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                                                                                                                                                                                                                                                                                                                              Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                   Comparative analysis of the whole set of rRNA operons between an enterchemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                      2 (sites)
Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                        Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S., Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T., Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                Hayashi,T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative chloride channel"
/protein id="BAB35721.1"
/db_xref="G1:13361765"
/tanslation="whichertheritypolarimerriliantyvgilaafavagerh
/translation="whicherthmerrilipalgglaagillagworftoorphap
amillewifinndsgsivnaatnispwrrilipalgglaagillaglasisscraorphap
TDYWEALQTOGOFDYAASIVKSIASILVYTSGSAIGREGAMILLAALAASCFAORFTP
                                                                                                           /gene="ECs2300"
                                                                                                                                                                                                                       /translation="melvmlkrffitgtdtsvgktvvsrallqalasqgktvagykpv
AKGSKETPEGLRNKDALVLQSVSTIELPYEAVNPIALSEEESSVAHSCPINYTLISNG
LANLTEKVDHVVVEGTGGWRSLMNDLRPLSEMVVQEQLPVLMVVGIQEGCINHALLTA
                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="BAB35722.1"
/db_xref="GI:13361766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1362. .2069)
/gene="ECs2299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1362. .2069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGAPGGVFTPTLFIGLAIGMLYGRSLGLWFPDGEEITLLLGLTGMATLLAATTHAPIM
STLMICEMTGEYQLLPGLLIACVIASVISRTLHRDSIYRQHTAQHS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWQLALGGLIVGLLSLFTPAVWGNGYSTVQSFLTAPPLLMIIAGIFLCKLCAVLASSG
                                                                              complement(2182. .3402)
                                                                                                                                                                                             QAIANDGLPLIGWVANRINPGLAHYAEIIDVLGKKLPAPLIGELPYLPRAEQRELGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINHSDALLYSVQLSVTVQARDYALIISTGVLAGLCGPLLLTLMNACHRGFVSLKLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQEWKLWIACGAAAGMAAAYRAPLAGSLFIAEVLFGTMMLASLGPVIISAVVALLVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="0157:H7"
/sub_strain="RIMD 0509952"
/note="similar to MLC_ECOLI gi|1787878 percent identity
in 406 aa (Conserved in E.coli K-12)"
                                                                                                                                                                         IRLAMLRSVLAVDRVTV"
                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ECs2299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Escherichia coli 0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to B1593_ECOLI gi|1787877 percent identity
9 in 235 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"similar to B1592_ECOLI gi|1787876 percent identity in 438 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="ECs2298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="ECs2298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:83334"
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AKPAAQPAA"
6798. .732
                                                                                                 /gene="ECs2304"
6798. .7322
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VMVTALLLASICTLLSTMMTSWHGILIMRALIGLSLSGVAAVGMTYLSEEIHPSFVAF
SMGLYISGNSIGGMSGRLISGVFTDFFNWRIALAAIGCFALASALMFWKILPESRHFR
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AVIVHEPLMAMIPHDHPLANNPNVTLAELAKEPFVFFDPHVGTGLYDDILGLMRRYHL
TPVITQEVGEAMTIIGLVSAGLGVSILPASFKRVQLNEMRWVPIAEEDAVSEMWLVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to ASR_ECOLI gi|1787881 percent identity
in 111 aa (Conserved in E.coli K-12)"
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/protein_id="BAB35723.1"
/db_xref="GI:13361767"
                                                                                                                                                                                                                                      KAAPAKTTHHKKQHKAAPAQKAQAAKKHHKNTKAEQKAPEQKAQAAKKHAKKHSHQQP
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VGLLSLAYLTGTWSSPKAGTMTTRYGRGPVMLFSTGVMLFGLLMTLFSSLWLIFAGML
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IGarllartnrsvlltaagkqfladsrqilsmvddaaaraerlhqgeagelrigftss
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/protein_id="BAB35724.1"
/db_xref="GI:13361768"
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LAQLRLNQSMSSMLHGQPLTVDSLCQAALRGDLLAKDIITGVGAHVGRILAIMVNLFN
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ASITKIVREMLEAHLVQELEIKEAGNRGRPAVGLVVETEAWHYLSLRISRGEIFLALR
/note="similar to B1598_ECOLI gi|1787882 percent identity 94 in 171 aa but differs at C-ter (Conserved in E.coli
                                                                  6798. .7322
/gene="ECs2304"
                                                                                                                                                                                                                                                                  /product="acid shock protein"
/protein_id="BAB35726.1"
/db_xref="G1:13361770"
/translation="MKKQIEGMTMKKVLALVVAAAMGLSSAAFAAETATTPAPTATTT
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/translation="MSRTTTVDGAPASDTDKQSISQPNQFIKRGTPQFMRVTLALFSA
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/protein_id="BAB35725.1"
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/transl_table=11
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99 in 417 aa (Conserved in E.coli K-12)"
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99 in 297 aa (Conserved in E.coli K-12)"
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/protein_id="BAB35727.1"
/db_xref="GI-13361771"
/ta_nsf="GI-13361771"
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VSNKGLWRYDIHDIEGRVDPTLGKRLKADGDGWIVPPAAAPWDFGLIVLRNPPSGITP
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100 in 109 aa (Conserved in E.coli K-12)"
/codon_start=1
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/gene="ECs2305"
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/gene="ECs2305"
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/sub_species="K12"
/db_xref="taxon:562"
/map="min 36.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="beta-lactam resistance
/protein_id="AAF82191.1"
/db_xref="GI:8953941"
/translation="MNRLIELTGWIVIVVSVII
/1 c 78 g 109 t
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A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map DNA Res. 3 (6), 363-377 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanal, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nahimoto, H., Nishio, Y., Oshima, T., Motomura, K., Nakamura, Y., Nakamura,
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Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The systematic sequencing of the Escherichia coli genome in Japan Unpublished

Japan 1 to 19211)
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Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda miniset
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Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Japan E.coli genome DNA sequencing group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Address: National Institute of Basic Biology, Okazaki, 444, Japan E-mail: kishorl@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Japan E.coli genome DNA sequencing project
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/clone_"Kohara clone #314"
/clone_lib="Kohara lambda miniset library"
/clone_Nucleotide position 1688148-1707358 from the
/note="Nucleotide position 1688148-1707358 from the
initiation site of ThrA (0 min.).-This clone is from
                                                                                                                                                                                       /map="36.3 min"
                                                                                                                                                                                                                                                                                /organism="Escherichia
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                      /db_xref="taxon:562"
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Genetic Info.; 8916-5
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/protein_id="BAA15364.1"
/db_xref="GI:1742667"
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/gene="fumA"
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/gene="fumA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mQKLINSVQNYAWGSKTALTELYGMENPSSQPMAELWMGAHPKS
SSRVQNAAGDIVSLRDVIESDKSTLLGEAVAKRFGELPFLFKVLCAAQPLSIQVHPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3260. .4435
/gene="manA, pmi"
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IHALALTKRAAAKVNEDIGLLSEEKASAIRQAADEVLAGQHDDEFPLAIWQTGSGTQS
NMNMNEVLANRASELLGGVRGMERKVHPNDDVNKSQSSNDVFPTAMHVAALLALRKQL
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                             /transl_table=11
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/db_xref="GI:1742669"
                                                                                                                                                                            /note="ORF_ID:o312#14
similar to [SwissProt Accession Number P32128]"
                                                                                                                                                                                                                                                                                                                                                                                                                              LISEFYPEDSGLFSPLLLNVVKLNPGEAMFLFAETPHAYLQGVALEVMANSDNVLRAG
LTPKYIDIPELVANVKFEAKPANQLLTQPVKQGAELDFPIPVDDFAFSLHDLSDKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HNSEIGFAKENAAGIPMDAAERNYKDPNHKPELVFALIPFLAMNAFREFSEIVSLLQP
VAGAHPAIAHFLQQPDAERLSELFASLLNMQGEEKSRALAILKSALDSQQGEPWQTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to [SwissProt Accession Number P00946]"
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RDIAHAKLKERMDNGEGLPQYIKDHPIYYAGPAKTPEGYASGSLGPTTAGRMDSYVDQ
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LIEAQNLGLGAQFGGKYFAHDIRVIRLPRHGASCPVGMGVSCSADRNIKAKINRQGIW
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PTCQDTGTAIIVGKKGQRVWTGGGDEAALARGVYNTYIEDNLRYSQNAPLDMYKEVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to [PIR Accession Number A03531]"
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MLCCQVMGNDVAINMGGASGNFELNVFRPMVIHNFLQSVRLLADGMESFNKHCAVGIE
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                                                                                                                                                                                                                                                  /gene="yihF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:1742668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Phosphomannose isomerase) (PMI) (Phosphohexomutase)."
/protein_id="BAA15365.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF_ID:0312#13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene≖"manA, pmi"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSNKPFHYQAPFPLKKDDTEYYLLTSEHVSVSEFEGQEILKVAP/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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/protein_id="BAA15363.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="Mannose-6-phosphate isomerase (EC 5.3.1.8)
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translation="MNKSLVAVGVIVALGVVWTGGAWYTGKKIETHLEDMVAQANAQL
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                                                             GCTAAGTAACATTTACCCCCTGAAGTTAATGGATC 215
                                                                                                                                                                                                CAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT 180
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                                                                                                                               Similarity
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/product="b-glucuronidase (EC 3.2.1.31) (GUS)
/product="b-glucuronoside glucuronosohydrolase)."
/product="b-glucuronoside glucuronosohydrolase)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7574. .
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/gene="uidA, gusA, gurA"
complement(8944. .10755)
/gene="uidA, gusA, gurA"
/note="ORF_ID:0314#3
similar to [SwissProt Accession Number P05804]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLAFLIGPSIKNSSPEEMVSVYHFWTIVLAIAGMVLYFIÖFKSTRENVVRIVAQPSLN
ISLQTLKRNRPLFMLCIGALCVLISTEAVSASSLEYNEYLVLDTGLFTYVLVLVQNLVG
TVASAPLVPGMVARIGKKNTELIGALLGTCGYLLFFWVSVWSLPVALVALAIASIGG
VTMTVWMALBADTVEYGSYLTGYRIEGLTYSLESFTRKGGQAIGGSIPAFILGLSGYI
ANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTDKKFKEIVVEIDNRKKVQQQ
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/db_xref="GI:1742670"
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/translation="MNQQLSWRTIVGYSLGDVANNFAFAMGALFILSYLVFWVLTD
AAGTMLLLVRVFDAFADVFAGRVVDSYNTRWGKFRPFLLEGTAPLMIFSVLVFWVLTD
WSHGSKVVYAYLTYMGLGLCYSLVNIPYGSLATAMTQQPQSRARLGAARGIAASLTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similar to [SwissProt Accession Number P30868]"
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Pred. No. 1.1e-42;
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l (bases 1 to 23009)

McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2
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Salmonella typhimurium LT2
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AE008763.1 GI:16419969
                                                                                                                                    Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programmer; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                     Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 23009)
The Salmonella typhimurium Genome Sequencing Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Salmonella.
EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/.and Pedro Romero and Peter Karp at EcoCyc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413 (6858), 852-856 (2001) 21534948
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n 67 of 220 of the complete
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone. The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset

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100.
                                                                                                                                                                                                                                                                                                                                   /organism="Salmonella typhimurium LT2"
/strain="LT2; SGSC 1412; ATCC 700720"
/db_xref="ATCC:700720"
                                                                            /note="similar to E. coli tyrosine tRNA synthetase
(AAC74709.1); Blastp hit to AAC74709.1 (424 aa), 968
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                       /codon_start=1
                                                         identity in aa 1 -
                                                                                                                 /gene="tyrs"
/EC_number="6.1.1.1"
                                                                                                                                                            /note="putative
100. .1374
                                                                                                                                                                                             /gene="tyrs"
                                                                                                                                                                                                                                        note="STM1449"
                                                                                                                                                                                                                                                         /gene="tyrs"
                                                                                                                                                                                                                                                                                                /note="LT2"
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:99287"
/product="tyrosine tRNA synthetase'
                /transl_table=11
                                                                                                                                                                                                                      . 93
                                                                                                                                                                              RBS
                                                                                                                                                                              for
                                                                                                                                                                            tyrs; RegulonDB:STMS1H001673"
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RESULT 10

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gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="glutathionine S-transferase"
/proteth_id="AAL20373.1"
/proteth_id="AAL20373.1"
/proteth_id="AAL20373.1"
/db_xref=="Gl:16419972"
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AVNPKGOVPALLLDGCTLLTEGVAIMOYLADSVPDRQLLAPVSSLARYHTLEWLNYIA
TELHKGETPLERPDTPETLKPAVRAGLEKKLOYVDESLSDDQMICGQRFTIADAYLFT
VLRWAYGVKLNNDGLTHLESYNQRVAKRPTVAAALKAEGLN"
comp_ment(2965...2970)
                                                    AVYLVKQLGMSEADSITLFSSESALVYGLVAIGGWLGDKILGTKRVIMLGAVVLAIGY
ALVAWSGHDAGIVYMGMAAIAVGNGLFKANPSSLLSTCYAKDDPRLDGAFTMYYMSVN
IGSEESMLATPWLAARYGWSTAFALSVVGMLITVVNFAFCQRWVKSYGSKPDFEPINF
                                                                                                                          /product="putative POT family peptide transport protein"
/protein_id="AAL20374.1"
/db xref="G1:16419973"
/translation="MSTANKKPTESVSLNAFKQPKAFYLIFSIELWERFGYYGLQGIM
                                                                                                                                                                                                                                                                         /note="similar to E. coli putative transport protein (AAC74706.1); Blastp hit to AAC74706.1 (500 aa), 90% identity in aa 1 - 498"
                                                                                                                                                                                                                                                                                                                                                          complement(3063.
/gene="ydgR"
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3063.
/gene="ydgR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to E. coli glutathionine S-transferase (AAC74707.1); Blastp hit to AAC74707.1 (201 aa), 84% identity in aa 1 - 200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2353.
/gene="gst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEHYFSATRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mknilaioshvveghagnsaaefpmrrlganvwplntvqpsnht
qygkwTgCvwppshlTeivqciadigqlahcdavlsgylgsabgeehilgivRqykaa
npoakyfcdpwghebkGcTvapgvaefhvkyaLpasbilabnlIeleiliskHsynn
ddavqaareliaqgpeivLykhlaragysserfemllyTaqeawhisrplydfgsrqp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="pyridoxal kinase 2"
/protein_id="AAL20372.1"
/db_xref="GI:16419971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number="2.7.1.35"
/Note="similar to E. coli pyridoxal kinase 2 ,
/Note="similar to E. coli pyridoxal kinase 2 ,
kinase (AAC74708.1); Blastp hit to AAC74708.1
90% identity in aa 2 - 287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMDIEEINALEEEDKNSGKAPRAQYVLAEQVTRLVHGEEGLVAAKRITECLFSGSLSA
LSEADFEQLAQDGVPMVEMEKGADLMQALVDAELQPSRGQARKTIASNAVTINGEKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIRKQVAPFLDFDCGENSAIAANNYDWFGSMNVLTFLRDIGKHFSVNQMINKEAVKQR
LNRDDQGISFTEFSYNLLQGYDFACLNKLHGVALQIGGSDQWGNITSGIDLTRRLHQN
QVFGLTVPLITKADGTKFGKTEGGAVWLDPKKTSPYKFYQFWINTADADVYRFLKFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mASSNLIKQLQERGLVAQVTDEDALAERLAQGPIALYCGFDPTA
DSLHLGHLVPLLCLKRFQQAGHKPVALVGGATGLIGDPSFKAAERKLNTEETVQEWVA
                                 RNLLLTIVGIVVLIAVATWLLHNQDIARMVLGVIALGIVIIFGKEAFSMHGAARRKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="gst"
/EC_number="2.5.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGVGDVTSGLLLVKLLQGATLQQALEHVTAAVYEIMIATKTMQEYELQVVAAQDRIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAL20371.1"
/db_xref="GI:16419970"
                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative RBS for gst;
complement(3063. .4577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="STM1451"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="pdxY"
                                                                                                                                                                                                                                                                                                                                                                                                              note="STM1452"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="pdxY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="pdxY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RBS for pdxY;
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(287 aa),
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Best Local
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     326
                                                                                                                                                                                                                                                                                                                                                                               Similarity
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146 AAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCTGAAG 205
CAGCCACCTGAACAGAGTGCTTCGGTACAACACAAGTAAGC
                                                                                                                                                           TTTATGGATAAATCAAAGCAAATGTCGTCAATAATGAATCGTCTTATTGAATTAACTGGG
                                                       TGGATAGTTCTCGTTATCTCAGTCATTCTTTTAGGTATTGCCAACCATATTGACAATTAC 12700
                                                                                                      TGGATCGTTCTTGTCGTTTCAGTCATTCTTCTTGGCGTGGCGAGTCACATTGACAACTAT 325
                                                                                                                                                                                                             TTAATGGATCAAGAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACAGGT 265
                                                                                                                                                                                                                                                                 AAAACGTTTCCCTCCCTCTTGCCGACCGTTCGCCAGGAAAGTAACATTTACCCCCCTG-TG 12820
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAL20376.1"
/db_xref="GI:16419975"
/db_xref="GI:16419975"
/t-zans1at.ton="MseIkdlyvoglukknusalvollgicphlavtstatnalgigla
/t-zans1at.ton="MseIkdlyvoglukknusalvollgicphlavtstatnalgigla
TTLVLTLTNLTVSALRRWTPAEIRIPIYVMIIASVVSAVQMLINAYAFGLYOSLGIFI
PLIVTMCIVVGRAEAFRAKKGFWLSALDGFSIGMGATGAMFVLGSLREILGNGTLFDG
ADSLLGGMAKVLRVEIFHTDSPFLLAMLPPGAFIGLGLMLAVKYLIDEKMKKRRAETA
PSAVPAGETGKY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to E. coli endonuclease III; specific for
apurinic and/or apyrimidinic sites (AAC74705.1); Blastp
hit to AAC74705.1 (211 aa), 95% identity in aa 1 - 211;
DNA glycosylase/apyrimidinic (AP) lyase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILAAIYNRMGDTLPMPMKFAIGMVLCSGAFLILPLGAKFANDAGIVSVNWLIASYGLQ
SIGELMISGLGLAMVAQLVPQRLMGFIMGSWFLTTAGANIIGGYVANLMAVPSDVTDP
LMSLEVYGRVFMQIGIATAVIAVLMLLTAPKLNRMTQDDDTAEKGSKAATV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5805.
/gene="ydgQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVPEDRAALEALPGVGRKTANVYLNTAFGWPTIAVDTHIFRVCNRTQFAPGKNVEQVE
EKLLKVVPNEFKVDCHHWLILHGRYTCIARKPRCGSCLIEDLCEYKEKVDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mnkakrleiltrlrdnnphpttelnftspfelliavllsaqatd
vsvnkataklypvantpaamlelgvegvksyiktiglfnskaenviktcrilldkhng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(6500. .7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5813. .5818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to E. coli orf, hypothetical protein
(AAC74704.1); Blastp hit to AAC74704.1 (231 aa), 91%
identity in aa 1 - 231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="endonuclease
/protein_id="AAL20375.1
/db_xref="GI:16419974"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to E. coli orf, hypothetical protein
(AAC74703.1); Blastp hit to AAC74703.1 (206 aa), 84
identity in aa 1 - 206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ydgP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="putative RBS for nth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="STM1454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ydq0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="STM1453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ydgR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="STM1455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                 22.2%;
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 106.6; DB Pred. No. 2e-17;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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'5.1"
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  366
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SOURCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill,J., Dougan,G., James,K.D., Thomson,N.R., Pickard,D., Wain,J., Churcher,C., Mungall,K.L., Bentley,S.D., Holden,M.T.G., Sebaihla,M., Baker,S., Basham,D., Brooks,K., Chillingworth,T., Connerton,P., Cronin,A., Davis,P., Davies,R.M., Dowd,L., White,N., Farrar,J., Feltwell,T., Hamlin,N., Haque,A., Hien,T.T., Holroyd,S., Jagels,K., Krogh,A., Larsen,T.S., Leather,S., Moule,S., O'Gaora,P., Parry,C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL627271 233050 bp DNA linear BCT 06-JUN-2002 Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 7/20.
AL627271 AL513382
AL627271.1 GI:16502733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, UK E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of S. typhi so
on the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 233050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 233050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/S_typhi/).
         VVSARAKNKRDVGRATLLAVLAALGIYLLVTLLSLGVLARPELAEMRNPSMAGLMVKM
MGPWGEIIIAAGLIVSVCGAYLSWTIMAAEVPFLAAAYKSFPGIFARQNAQGAPSASL
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LVIVFSALSFFTDTPALRLFGDGNTWQAIVGASVLLMIVHFLILRGVQTAASINLVAT
LAKLLPLGAFIVLAIMMFKLDTFTLDFTGVELGIPVWBQVKNTMLITLWVFIGVEGAV
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/protein_id-"CAD01890.1"
/db_xref-"GI:16502734"
/db_xref-"SPTREMBL:08XGG1"
                                                                                                                                                                                                                                                                                                                                                                                 Orthologue
                                                                                                                                                                                                                                                                                                                                                                                                                           arginine/ornithine antiporter arcD SW:ARCD_PSEAE (P18275) (482 ma) fasta scores: E(): 0, 45.5% id in 479 ma Fasta hit to YJDE_ECOLI (445 ma), 31% identity in 450 ma
                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                        (460 aa), 93% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="STY1645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Salmonella enterica subsp. enterica serovar
≀vohi"
                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Similar to Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="STY1645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            typhi sequencing
                                                                                                                                                                                                                                                                                                                                                        of E. coli ARCD_ECOLI; Fasta hit to ARCD_ECOLI 93% identity in 460 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at
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                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Similar to Staphylococcus aureus response regulator YycF yycF TR:Q9XCM7 (EMBL:AF136709) (233 aa) fasta scores: E(): 8.8e-28, 37.6% id in 234 aa Fasta hit to TORR_ECOLI (230 aa), 31% identity in 213 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="Sptrembl:Q826S2"
/translation="mglvikaalgalvvvligllsktknyyiaglipleptealiahy
ivasergidamrttivesmwsiipyeiylatlmyesgvmrlpvalggavvcwglsawl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Orthologue of E. coli YDGC_ECOLI;
YDGC_ECOLI (111 aa), 81% identity in 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1643. .1978)
/gene="STY1646"
                                                                                                                                                                                                                                                                                                                                                                                                /gene="ST1647"
/gene="Ffam match to entry PF00072 response_reg, Response
/note="Pfam match to entry PF00072 response_reg, Response
/mulator receiver domain, score 62.70, E-value 7.9e-15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="Sptrembl:Q8Z6S1"
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/translation="mmrivfyeddabygsliaaylakhdidviveprgdraedlility
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Tppayvllarlrhhqqsimdrdallktirgvnydgldrsvdvaisrlrkklldsaa
Slstadfellwelathagqimdrdallktirgvnydgldrsvdvaisrlrkklldsaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orthologue of E. coli rstA (RSTA_ECOLI);
RSTA_ECOLI (242 aa), 85% identity in 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fasta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fasta hit to YEDW_ECOLI (239 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fasta hit to YLCA_ECOLI (227 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fasta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STY1647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="STY1647"
/note="rstA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative membrane protein"
/protein_id="CAD01891.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY1646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="STY1645"
                                                                                                                                                                                                                                                                                                                                                                                        regulator receiver 2582. .2794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                           complement(2901. .3260)
/gene="STY1648"
                                                                                                                                                                                                                                                                                         Transcriptional regulatory 62.90, E-value 1.8e-17"
                                                                                                                                                                                                                                                                                                                     ysuce"Pfam match to entry pF00486 trans_reg_C, /notee"Pfam match to entry protein, C terminal, Transcriptional regulatory protein, C terminal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPYRIKTIRNKGYLFAPHAWDETTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                          /product="hypothetical
/protein_id="CAD01893.:
/db_xref="GI:16502737"
                                                                                                                                                                                                                                                                     complement(2901. .3260)
                                                                                                                                                                                                                                                                                                                                                               /gene="STY1647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                   /db_xref="SPTREMBL:Q8Z6S0"
                                                                                                                     /transl_table=11
                                                                                                                                              /codon_start=
                                                                                                                                                                    /note="No significant database matches"
                                                                                                                                                                                                                                          /gene="STY1648"
translation="MNQRHPNLNNIISANANFSYMLLINTKVTIGNAYIYGEYVCYYI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hit to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hit to CPXR_ECOLI (232 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAER_ECOLI (240 aa),
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                                                                        nı protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (239 aa),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identity
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aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fasta hit to
aa overlap"
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aa

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Matches 148;
                                                                                                                                                                                                                                                                                           Query Match
17956 AGCAAATGTCGTCAATAATGAATCGTCTTATTGAATTAACTGGGTGGATAGTTCTCATTA 18015
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                           222 GAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACAGGTTGGATCGTTCTTGTCG 281
                                                                                                                                                    Local Similarity
                                                                                                                  TCTTGCCGACCGTTCGCCAGGAAAGTAACATTTACTCTCTG-TGTTTATGGATAAATCAA
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFGDYGSFDYGRNYGVLYDVEGWTDMLPEFGGDSYTYADNYMTGRANGVATYRNTDFF
GLVDGLNFALQYGKNESQSADDVNLGTNNRNNGDDI RYDNGDEFGISTTYDIGMGFS
AGAAYTTSDRTNEQVNAGGTIAGGDKADAWTAGLKYDANLYLATMYSETRNMTPYGK
TDKGYDGGVANKTQNFFVTAQYQFDFGLRPAVSFLMSKGKDLTYNNVGDDKDLVKYA
DVGATYYFNKNFSTYVDYKINLLDDDDFFYKDAGISTDDIVALGMVYQF
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3317. .4468
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GLFRLIKIALMYTVSVF"
                                                                                                                                                                                                                                                                                                                                                   RWSIAHLNTGSPQTLERWRKLGLAYTVQMGPYFEGLAIRDANPPGATDNSPPVRLALD
KGLVVAGGTDSTRIGIAGVWHAIEYHITGIASGGSVRKPASERLTRLEALALYTRHAA
WLAFAEQHRGQLSVGKQADLAVLNQPFMTMPEDRIDTIRAVLTLVDGRIVHESPDLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSHALPDHPAYIQYLYDYALVNQRGIDVLGLNDTPPPDLAGIRVERDAKGSATGKLFG
DIAAFNQLFASISSNADREGGLRQFFADMNARGVTGIIDPSAGPAAAYEPLFAMRNQG
DLPLRVGYRIPVQPEAKGHEAQWFSNLMAFRPARADDGQLAFLGLGESLVAGMNDGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00267 Gram-ve_porins, General
diffusion Gram-negative porins, score 619.80, E-value
6.8e-189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT:056111"
/translation="MKRKVLALVIPALLAAGAAHAAEIYNKDGNKLDLYGKVDGLHYF
SDDSSKDGDQTYMRVGFKGETQINDQLTGYGQWEYNVQANTTEGEGANSWTRLAFAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthologue of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mlmislvpptlsxfallflltatgaataarpaadiilhngniit
LNDAQPQASALAISGSRIVAIGDDTATNEWRGDHTRTIDLQGKTVIPGLTDTHIHAIR
GGQTWTFETYWYDSPSLKDALDKLRADANRRPHDQWVAVVGSWIPAQFAENRASTVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Similar to Mycobacterium tuberculosis hypothetical 57.3 kDa protein rv0552 or mtcy25d10.31 TR:006418 (EMBL:295558) (534 aa) fasta scores: E(): 1.8e-20, 26.4% id in 561 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="outer membrane protein"
/protein_id="CAD01894.1"
/db_xref="GI:16502738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fasta hit to NMPC_ECOLI (365 aa), 63% identity in 390 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fasta hit to YEDS_ECOLI (397 aa), 67% identity in 401 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 aa overlap
Fasta hit to PHOE_ECOLI (351 aa), 61% identity in 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPGFSSSEQDKTALRQVATFAAKRGIPLEIHAYTDDSADAILTIFEQVAQQYDLRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAD01895.
/db_xref="GI:16502739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4621. .6327
/gene="STY1650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="STY1649"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY1649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q8Z6R9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Fasta hit to OMPC_ECOLI (367 aa), 66% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="STY1650"
                                                                                                                                                                                                                                                                21.5%;
                                                                                                                                                                                                                        Score 103.4; Db 1,
Pred. No. 1.2e-16;
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                                                                                                                           Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sitrauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Titrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Bireot, Submigston, M., and Zody, M., Direot, Submigston, M., Submon, J., Ve, M.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Direot, Submigston, M., Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Submon, J., Ye, W.J., Ye, W.J., Young, G., Zainoun, J., Submigston, M., Submigston, M., Submon, J., Ye, W.J., Young, G., Zainoun, J., Submigston, M., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N. Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-137P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                  Direct Submission
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(24-AUG-2002) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence the available and the accession number will
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                     Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Blg Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 154868 bases at least Q40 Consensus quality: 159752 bases at least Q30 Consensus quality: 159752 bases at least Q30 Consensus quality: 161420 bases at least Q30 Consensus quality: 161420 bases at least Q30 Consensus quality: 161420 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L10489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
     Insert size: 155000; agarose-fp Insert size: 162284; sum-of-contigs Quality coverage: 4.4 in Q20 bases; Quality coverage: 4.2 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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    Genome Center

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108092 127851: contig of 19760 bp in
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11878 14570: contig of 2693 bp in
14571 14570: gap of 100 bp
14571 14570: gap of 2852 bp in
17523: contig of 2852 bp in
17523 17622: gap of 100 bp
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5093 7181: cor
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     /note="assembly_fragment"
14671. .17522
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/db_xref="taxon:9606"
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11777: contig of 2452 bp in
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17: gap of 100 bp
4992: contig of
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dq

bp in length

length length

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is as soon as it is available and the accession number will 1 2073: contig of 2073 bp in length 2074 2173: gap of 100 bp 2174 3577: contig of 1404 bp in length

100

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length

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BASE COUNT
ORIGIN
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ORGANISM
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Mammalla; Butherla; Primaces, ....
1 (bases 1 to 167577)
1 (bases 1 to 167577)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Birren,B., Cintonosome 11, clone CTD-2507G9
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhqalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gerereira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K., Johnson, R., Laroque, K., Karatas, A., Kells, C., Laroque, K., 
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167577 bp DNA linear PRI 12-JUN-2 Homo sapiens chromosome 11, clone CTD-2507G9, complete sequence AC099687
                                                                                                                                                                                                                                                                                                                                                       Unpublished
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59320. .70858
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25643. .31250
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154051. .164184
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TITLE

JOURNAL

AUTHORS

JOURNAL

Center: Whitehead

Institute/ MIT Center for Genome Research

AUTHORS

JOURNAL TITLE

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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrin, J.,
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Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triylilo,J., Vassiliev,H., Topham,K., Travers,M., Travis,N., Triylilo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainon,J., Zembok,L., Zimmer,A. and Zody,M.
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Alderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Alderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Faro, S., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-plerre, N., Hagos, B., Horton, L., Hulme, W., Illey, I., Grand-plerre, N., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Landarares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Marquis, N., Marquis, N., Marquis, N.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkly,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
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                                                                                                                                                                                                                                          Submitted (12-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 12, 2002 this sequence version replaced gi:17386347.
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Direct Submission
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Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mienga,V., MurphyT., NayJor,J., Ngyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                               All repeats were identi
                                                          A.F.A. & Green, P. (1996-1997)
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12862
Center clone name: 2507_G_9
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complement(9197. 9374)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTATACTTGAAACTAAAAATACATGTAAGCAAACAGAAAAAATACATATAAAA 65717
      Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Conserv
                                                                             Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 2, 2002 this sequence version replaced gi:21655322.
                                                                                                                                                                                                                                                                                                                             AL591126 190015 bp DNA linea:
Mus musculus chromosome 11 clone RP23-188A3, ***
PROGRESS ***, 2 unordered pieces.
                                                                                                                                              Submitted (28-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                        AL591126.16 GI:21665917
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                              Center: Wellcome Trust Sanger Institute
                                                                                                                                                                  Direct Submission
                                                                                                                                                                                  Phillimore, B.
                                                                                                                                                                                                                Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                             karyota; Metazoa; Chordata;
nmalia; Eutheria; Rodentia;
(bases 1 to 190015)
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29912. .29965
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complement(23783. .2
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/rpt_family="MIR"
                                http://www.sanger.ac.uk
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complement(2.115)
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22008. .22232
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25318. .25403
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Project Information
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                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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0;

Gaps

0

HTG 29-JUN-2002

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BASE COUNT
ORIGIN
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Search completed: February 7, 2003, 20:36:34 Job time : 2920 secs
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Best Local Similarity 58.3%;
Matches 74; Conservative
                                                                                                                                                                                                              21437 ATTGTATTATTGTTATTGTTACATAGCATTAACCATCTTTTCTAAGAAGGAAAATATAT 21496
                                                                      21497 AGAGCTG 21503
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111249. 190015
/note-"assembly_fragment:07880.1"
60196 a 40379 c 37523 g 51817 t 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 111148: contig of 111148 bp in length
111149 111248: gap of 100 bp
111249 190015: contig of 78767 bp in length.
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/db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP23-188A3"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .190015
                                                                                                                                                                                                                                                                                   Score 42.2; DB 2; Length 190015; Pred. No. 1.3; 0; Mismatches 53; Indels 0;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ABA90521
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Genomic sequence o
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7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9
198285	198285	66109	66109	17959	17959	11955	10776	6030	6030	5304	20209	19139	19139	243	2202	2181	785	785	32189	32189	8577	6123	15399	7536	1830121	822	822	7053	6310	6310	6310	5914	15456	15456	15881
24	24	24	24	24	24	23	23	24	24	24	22	22	22	21	24	24	24	24	23	22	24	24	24	24	17	24	24	22	24	24	24	24	24	22	24
ABN97319	ABK84699	ABL62723	ABN97273	ABL32574	ABL54341	ABL30298	ABL03804	ABK28311	AAS61347	ABL34018	AAK81223	AAK81225	AAK81224	AAC12247	ABN66876	ABN71144	ABQ30143	ABQ30142	ABL97577	AAL04670	ABL33787	ABL32821	ABL33515	ABL33464	AAT42063	ABQ36727	ABQ36726	AAS26613	ABK31364	AAS61268	ABL70321	ABL34168	AAD27766	AAC85009	ABK31182
Gene #3817 used to	Human cDNA differe	Colon adenocarcino	Gene #3771 used to			Drosophila melanog	Drosophila melanog	DNA transcription	Human gene regulat					Human secreted pro	Streptococcus poly			=		reprod	immune	immune	immune				Oligonucleotide fo	Human cDNA encodin	Signal transductio		Chemically treated	Human immune syste	Bovine parainfluen	₼	Signal transductio

ALIGNMENTS

RESULT 1 ABA02070

ABA02070 standard; DNA; 481

ВР

11-FEB-2002 ABA02070;

(first entry)

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mutation
                                                                            misc_signal
                                                                                                                                                primer_bind
                                                                                                                                                                                                     Beta-lactam resistance; blr gene; Beta Lactam-358; BLR; transmembrane; efflux pump; periplasm; peptidoglycan synthesis inhibition; drug discovery; screening; antibiotic; antibacterial; vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                            Escherichia coli beta-lactam resistance (blr) gene
                                                                                                               promoter
                                                                                                                                                                                 Escherichia coli.
                                  replace
/*tag=
                                                                                                      /*tag- a
/note= "Primer F2 (not given in the specification)"
131..161
                                                                                                                                           Location/Qualifiers complement (107..125)
                                           /note= "Transcription initiation site"
replace (214..217, CTAG)
                                                                                        /*tag= b
/label= blr_promoter
              /note=
                                                                  ′*tag=
- Amber_mutation_Q13
"An amber mutation at this position does not
abolish beta-lactam resistance"
                                                                     a
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This sequence represents a beta-lactam resistance (blr) gene from Escherichia coli. The blr gene encodes a 41 amino acid transmembrane protein (also designated Beta Lactama 358 in the specification) with a molecular weight of 4556 Daltons which confers resistance to beta-lactam antibiotics. The blr gene was initially identified in a 602 bp hypothetical intergenic region of the genome of an antibiotic-susceptible strain of E. coli, RW553. In the RW583 strain, the blr gene is disrupted by insertion of the transposon mini-Taphoa. A clone bearing an ORF (open reading frame)-containing 358 bp segment of the "intergenic" region was found to restore beta-lactam resistance in RW358. Certain amber mutations introduced into the 358 bp clone were found to abolish beta-lactam resistance and resistance could be restored using an amber suppressor, indicating that a protein encoded by the clone was responsible for mediating beta-lactam resistance. It is suggested that
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                                                                                                                                                                                                                                               New membrane protein, designated Beta Lactam-358 polypeptides, that affect susceptibility to antibiotics which affect peptidoglycan synthesis in microbes, useful for identifying modulators for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
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P-PSDB; AAM52607.
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14-JUL-2000; 2000US-218380P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001
                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                         (TUFT )
                                                                                                                                                                                                                                                                                                                                                                          TUFTS COLLEGE
                                                                                                                                                                                                          Fig 1A-B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                               McMurry LM;
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/*tag= :
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Primer
470..481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Primer R3 (not given 338.339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "BLR protein" replace (247..249, TAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448..465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoter for 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An amber mutation at this posit abolish beta-lactam resistance"
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"An amber mutation at the beta-lactam resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amber_mutation_V20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using an amber suppressor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using an amber (292..294, TAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (235..237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter for ORF71 (putative histone-like negative regulator gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on point for mini-TnphoA transposon strain RW583"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the BLR protein may act by increasing a beta-lactamase activity in a cell, possibly being a component of an uncharacterised membrane-bound efflux pump capable of expelling beta-lactams from the periplasm. The BLR protein may be used in methods to identify compounds that modulate antibiotic resistance in a bacterium. The BLR protein, gene, BLR agonists or antagonists, and anti-BLR antibodies may be used to treat bacterial infection, particularly by an organism resistant to antibiotics that affect peptidoglycan synthesis. They may also be used in screening assays, in vaccines, and in diagnostic assays. BLR nucleotides are useful in gene therapy applications to modulate BLR expression, and to detect BLR expression in a biological sample.
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481
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                                             421
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                                                                                                                                                                                                                                                                                                                                                                           TGCCTCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTT
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                                                                                                                                                                                                                                                                                                                  TGCCTCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCCACGCTCAACAGTTT
                                          A 481
                      A 481
                                                                                       GTAAGCTCTGCACTTGTGGAGCGACATGCTGCCCGTCCGGGTGCATGTTTTCACTTGTCG
                                                                                                                                     CGTGGCGAGTCACATTGACAACTATCAGCCACCTGAACAGAGTGCTTCGGTACAACACAA
                                                                                                                                               CGTGGCGAGTCACATTGACAACTATCAGCCACCTGAACAGAGTGCTTCGGTACAACACAA
                                                                                                                                                                                                                              481;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                           Score 481; DB 24;
pred. No. 1.7e-129;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 481;
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RESULT 2
ABA90521/c
ID ABA90521 standard; DNA; 2365589 BP.

XX
AC ABA90521;
XX
DT 16-MAY-2002 (first entry)
XX
DE Genomic sequence of Lactococcus lactis IL1403.
XX
Biosynthesis; biodegradation; lactic bacterium;
XX
OS Lactococcus lactis IL1403.
XX
PD FR2807446-A1.
XX
PD 12-OCT-2001.
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yogurt;

cheese;

gb

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RESULT ABK3131:
ID ABK313:
ID ABK31
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Best Local :
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ABK31312
                                                                                                                                                                                                                                                                 Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention helps research in lactic bacteria, production of yogurt and cheese.

Note: The sequence data for this matter in this matter in the sequence data for the sequence d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence, particularly to identify Lactococcus lactis related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000;
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                                                  WO200200926-A2
                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAAC 128
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ilarity 47.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 6294 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 3;
0; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                    cytosine methylation state;
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Query Match
                                                                                                                                                                                  for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31545 represent chemically pretreated genomic DNA cancer.
                                                                                                                 their complementary sequences. Note: The sequence data for this specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                           signal transduction associated genes. The DNA sequences are chemical modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
01-SEP-2000;
                                                                    Sequence 6294 BP;
                                                                                                                                                                     sequences of different genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                               The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-2001;
                                                                                                      European Patent Office.
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                 Local
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes associated with signal transduction
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2000DE-1043826
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                                                                    1727 A; 189 C;
                 8.1%;
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                 Score 38.8;
Pred. No. 0
                                                                                                                    n patent did not form in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                             chemically modified DNA equences
                                                                    1480 G;
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                                  DВ
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                                  Length 6294;
                                                                    other;
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                                                                                                                                                                                                                                                                                                                                                                                                                             sequences
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Matches 146 AAAACCTCAGTAAAAATC 163 788 26 TTGTTTAACTTAAGTCAAAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCA ATTTGACACTATCCTTTACCCACGCTCAACAGTTTAATAACCTGCCAGCAATAAGGGATG TAATTAAAACAAATAAAAAAAAAAACGTAACCTCCAACATATAAAACGTAAACATATAC 76; Conservative 0; Mismatches 62; Indels 0; Gaps 729 85

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668 TAACCCACAAAAAAAAAAC

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ABL32368/c
ID ABL323
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AC ABL323
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XX
A RESULT ABL32368 standard; DNA; 9997 26-MAR-2002 ABL32368; (first entry) system associated ВP gene SEQ

Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

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RESULT 5
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ID ABL34484;
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DT 26-MAR-2002 (first of the text)
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 341; 32pp + Sequence Listing;
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79; Conserv
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                                                                                                                            is associated methylation;
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                                                                                                                                  cytostatic;
ds.
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                                                                                                                                                            therapy;
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ID ABK315
XX ABK3151/c
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XX 23-APR
XX Signal
XX Human;
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KW antitu
XX Homo s
OS Synthe
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                         Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                         Signal transduction associated gene modified complementary DNA #177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9997 BP; 2290 A; 91 C; 2181 G; 5435
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                                                                     29-JUN-2001; 2001WO-EP07472
                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    GCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTTCCAACGAACAAAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-010922/01
                                                                                                                                                                                                                                                                                                                                                        АААААТААСТАААААААААААТАА 5778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS AG
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                   2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                47108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from chemically treated cancers by analysis of cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.8;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         χ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
.77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asis genes,
methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9997;
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(EPIG-)

EPIGENOMICS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK3158-ABK31545 represent chemically pretreated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal transduction associated genes. The DNA sequences are chemical modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              their complementary sequences.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 354; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                       WO200202807-A2
                                                                                                                                             Cell signalling;
                                                                                                                                                                               Chemically treated cell signalling DNA sequence#17.
                                                                                                                                                                                                                      01-JUL-2002
                                                                                                                                                                                                                                                                                           ABL70143 standard; DNA; 15881 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47108 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences of different genes associated with signal transduction, or
                    10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to chemically modified DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAAAACAAAAAACTATAAAAAATCCCAAAATTAAACAAACATATAAAATTTCCCTAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAAAACCTCAGTAAAAAT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCACGCTCAACAGTTTAATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCA 102
                                                                                                                                                                                                                                                                                                                                                                                    ACCCAATTAACCACTTAAAATCCATCTTAAAAAATTAACTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                         AGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACACCCAACCCAAACTTACTTAATTCTAATTAACTAATTAACTAATTCAAACAAATATA 19049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                  (first entry)
                                                                                                                                             cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15349 A; 429 C; 8736 G; 22594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.0%;
48.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 116;
                                                                                                                                             cell signalling disease;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                    266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 8
ABL32260/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is CC provide the chemically modified DNA of genes associated with cell CC signalling, as well as oligonucleotides and/or PNA-oligomers for CC detecting cytosine methylations, as well as a method which is CC particularly suitable for the diagnosis and/or therapy of genetic and CC epigenetic parameters of genes associated with cell signalling. The CC chemically modified DNA provided by the invention is useful for diagnosis CC and therapy of diseases such as solid tumours and cancer. The sequences CC genemic DNA's of genes associated with cell signalling.

CC Note: The sequence data for this patent is not represented in the printed constitution, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                         14445
                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 33; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic environces of rances associated with cell signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
                                             antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia, Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2001; 2001WO-EP07471
                               gene;
                                                                                                                                                                                                                                                                                        ABL32260 standard; DNA; 15881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15881 BP; 4515 A; 204 C; 3588 G; 7574 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-)
                                                                                                                  neuroprotective;
                                                                                                                                                                                   Human immune
                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                      ABL32260
                                                                                                                                                                                                                                                                                                                                                                                                           222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 AAAAAAATAGCGAATTTTCCAACGAACAAAAAGCTAAATATCGCAAAAAACCTCAGTAAAAA 161
                                                                                                                                                                                                                                                                                                                                                                                            GAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-154758/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signalling e.g. cancer, comprises chemics of genes associated with cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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2000DE-1043826
                                                                                                                                                                                  system
                                                                                                                                                                                                                   (first entry)
                                                                                                               anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG
                                                                                                                                                                                  associated gene SEQ
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Pred. No. 1
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                                                                                                                                                                                   NO:
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Homo sapiens

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RESULT 9
AAS61069/c
ID AAS610
XX AAS610
XX AAS610
XX 29-JAN
DT 29-JAN
XX Human;
XW Human;
XW cardia
KW renal
KW nephro
XX Homo s
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               14565 AAAACAAAATCAAAAACAACAACAAAAAAAACACTAAATAAATAACGAAAAAACCACCAAC
                                                                                   colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthma
nephrotropic; gynecological; anti-tumour; immunosuppressive; cytos
                                                                                                                          cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
  18-OCT-2001
                                                                                                                                                                                                 Human gene regulation-associated gene oligonucleotide #24.
                                                                                                                                                                                                                               29-JAN-2002
                                                                                                                                                                                                                                                                                   AAS61069 standard; DNA; 15881 BP
                              WO200177375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15881 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 AAAAAAATAGCGAATTTTCCCAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis heumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis and treatment of diseases associated with abnormal osine methylation -
                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                                                                                                     AATATATCTATTTTTTAAATAAACTCCTTATACTTTTAATA 14405
                                                                                                                                                                                                                                                                                                                                                                               GAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACA
                                                                                                                                                                                                                                                                                                                                                                                                         Gene regulation-associated gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 233;
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                                                                                                                                                                                                                             (first entry)
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2000DE-1043826
                                                                                                                                                       inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4515 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.98;
52.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3588 G;
                                                                                                                                                                   severe combined immunodeficiency;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7574 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
                                                                                                coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15881;
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ABK31182/c
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WXEX DX ACX ID
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AATATATCTATTTTTAAATAAACTCCTTATACTTTTAATA 14405 GAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACA 262 14446

0;

222

Signal transduction associated gene modified DNA #13

signal

transduction associated

gene;

cytosine methylation state

23-APR-2002 ABK31182

(first

entry)

ABK31182 standard; DNA; 15881

ВP

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                                                                                                                                                                                                                                                                                                     CC 18 bases of a chemically pretreated gene associated with gene regulation contents of the contents of conten
                                                                                                                                                    Matches
                                                                                                                                                                                                Query Match
                                                            06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek
                                                                                                                                                                                                                                             Sequence 15881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ
                                                                                                    102 AAAAAAATAGCGAATTTTCCCAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAA 161
                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001;
                                                                                                                                                                            Local
A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-017470/02
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relates to 224 nucleic acid sequences comprising at least
                                                                                                                                                                                                                                             BP; 4515 A; 204 C; 3588 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                        7.9%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin
                                                                                                                                                  0;
                                                                                                                                                                        Score 37.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ζ.
                                                                                                                                                                                                DB
                                                                                                                                                                                                                                         7574 T;
                                                                                                                                                                                             24;
                                                                                                                                                  77;
                                                                                                                                                                                             Length 15881;
                                                                                                                                                                                                                                           0 other
                                                                                                                                                  Indels
                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulation
                                                                                                                                                  Gaps
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RESULT 11
AAC85009
ID AAC85
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AC AAC85
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                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or consisted genes. The DNA sequences are chemically disulphite. Also disclosed are oligonuclectides and/or PNA oligoners of credetecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and cepigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, bloodisting such as tissue from cerebral-spinal fluid, tissue embedded in parafifin such as tissue from ceyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, thistologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of cancer. ABK31189-ABK31545 represent chemically pretreated genomic DNA cancer of different cancer.
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                            14565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CpG island; signal transduction associated disease; solid tumour; cancer;
antitumour; cytostatic; mutant; ds.
                     AAC85009
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15881 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200926-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                   AAC85009 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences of different genes associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001; 2001WO-EP07472
                                                                                                                                                                                                                                                                                       102 AAAAAAATAGCGAATTTTCCCAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAA 161
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                             GAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACA
                                                                                                                                                                                                                                                         sapiens
                                                                                                                             AATATATCTATTTTTAAATAAACTCCTTATACTTTTAATA 14405
                                                                                                                                                                                          1; SEQ ID No 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary sequences
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                          Conservative ·
                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                       4515 A; 204 C; 3588 G; 7574 T; 0 other;
                                                                                                                                                                                                                                                                                                                                     7.9%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24pp; English
                                                   15456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                       Score 37.8;
Pred. No. 1
                                                 вр
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with signal transduction, or
                                                                                                                                                                                                                                                                                                                                       .8
                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                          77;
                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                       Length 15881
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              14446
                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                          RESULT 12
AAD27766
ID AAD27
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                          3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus (PIV) that is infectious and attenuated in humans. The virus comprises a major nucleocapsid protein, a nucleocapsid phosphoprotein, a large polymerase protein, and a partial or complete PIV background genome, or antigenome of a human PIV (HPIV) or bovine PIV (BPIV), combined with one or more heterologous gene(s) or genome segment(s) of different PIV to form a human-bovine chimeric PIV genome or antigenome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
   Parainfluenza virus;
                                                                                                                                                                                                           4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The chimeric PIV is useful in attenuated vaccines to elicit immune response against one or more virus(es) selected from HPIVI, HPIV2 and HPIV3 and most preferably against HPIV3. The present sequence represents the nucleotide sequence of bovine PIV3 SF strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human-bovine chimeric parainfluenza virus (PIV), useful in an attenuated vaccine to elicits an immune response against one or more virus(es) selected from human PIVI (HPIVI), HPIV2 and HPIV3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt AC,
Durbin AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200104320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parainfluenza virus; PIV; infectious; human; nucleocapsid protein; nucleocapsid phosphoprotein; polymerase protein; human; bovine; HP: chimeric; vaccine; immune response; HPIV1; HPIV2; HPIV3; BPIV3; ds
                               Bovine parainfluenza
                                                              18-APR-2002
                                                                                              AAD27766;
                                                                                                                                                                                                                                                                                                                                     3926 AATGGAAAGGTCAAAAGACAGGTATGGGAGCATAAGTGATCTAGATGATGATCCAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15456 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated human-bovine chimeric parainfluenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7A-G; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine parainfluenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2001 (first entry)
                                                                                                                             AAD27766 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                                                                          328
                                                                                                                                                                                                                                                                                                                                                                      AATGGATCAAGCAGAGAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACAGGTTG
                                                                                                                                                                                                                                         GCCACCTGAACAGAGTGC 345
                                                                                                                                                                                                                                                                        CAAGGTTTGTGGCTCTGGATCATTGCCACTTGGGTTGGCTAGATACACTGGAAATGATCA
                                                                                                                                                                                                                                                                                                      GATCGTTCTTGTCGTTTCAGTCATTCTTTGTTGGCGTGGCGAGTCACATTGACAACTATCA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-081053/09.
                                                                                                                                                                                                           GGAACTCCTACAGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US17066
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                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0143134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5872 A; 2656 C;
                                                                                                                               DNA; 15456
                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%;
54.3%;
PIV; nucleocapsid protein;
                               virus 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MH,
                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37.2;
Pred. No. 2.
                               (BPIV3) SF DNA
                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins PL,
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain
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DB 2.6; <u>ც</u>

63; 22;

Indels Length 15456

0;

Gaps

0;

3985

267

4045

polymerase protein;

3993 T; 0 other;

Murphy BR,

Bailly JE;

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RESULT 13
ABL341
XX
ABL341
AC ABL341
XX
Z6-MAR
XX
DT 26-MAR
XX
DE Human
XX
Human
XX
Human;
KW antlar
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viruses (PIV) that are infectious and attenuated in humans and other memmals. The viruses comprise a major nucleocapsid protein (N), a nucleocapsid phosphoprotein (P), a large polymerase protein (L) and a partial or complete PIV background genome or antigenome of a human PIV (HPIV) or bovine PIV (BPIV), combined with one or more heterologous genes or genome segments of a N, P, L, or M gene of a different PIV to form a human-bovine chimeric PIV genome or antigenome. The invention also relates to methods and compositions incorporating human-bovine chimeric PIV for prophylaxis and treatment of PIV infection. The chimeric PIVs are useful in attenuated vaccines to elicit an immune response against one or more viruses selected from HPIV1, HPIV2 and HPIV3. The present sequence is bovine parainfluenza virus 3 (BPIV3) SF DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPIV; human PIV; nucleocapsid phosphoprotein; bovine PIV3; BPIV3; prophylaxis; infection; vaccine; immune response; immunostimulant virucide; SF DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human-bovine chimeric parainfluenza virus (PTV), useful attenuated vaccine to elicits an immune response against one or virus(es) selected from human PTV1 (HPTV1), HPTV2 and HPTV3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skiadopoulos MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2000; 2000US-215809P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine parainfluenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 2; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                           3926 ANTIGGAAAGGTCAAAAGACAGGTATGGGAGCATAAGTGATCTAGATGATGATCCAAGTTA 3985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to chimeric human-bovine parainfluenza
                                                                                                                                                                   ABL34168 standard;
                                                                                                                                                                                                                                                4046 GGAACTCCTACAGGCTGC
               antiarteriosclerotic;
                                                               Human immune system associated
                                                                                                   26-MAR-2002
                                                                                                                                    ABL34168
                                                                                                                                                                                                                                                                                                             3986 CAAGGTTTGTGGCTCTGGATCATTGCCACTTGGGTTGGCTAGATACACTGGAAATGATCA
     neuroprotective;
                                                                                                                                                                                                                                                                                                                                   268 GATCGTTCTTGTCGGTCATTCATTCTTGGCGTGGCGAGTCACATTGACAACTATCA 327
                                                                                                                                                                                                                                                                               328 GCCACCTGAACAGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                      AATGGATCAATCAAGAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACAGGTTG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                         75; Conser
                                   immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US21527
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
     otic; antianaemic; cytostatic;
anti-HIV; anticonvulsant; oph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5871 A;
                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.78;
54.38;
                                                                                                                                                                    5914
                                                                                                                                                                                                                                                  4063
                                                                                                                                                                                                                                                                                345
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Pred. No. 2
                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERVICES
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                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2936 G; 3996 T; 0 other;
                                                                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.
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                                                                     NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmidt
   ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                     2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15456
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 14
ABL703211/c
ID ABL70
XX ABL70
AC ABL70
XX DT 01-JU
XX Chemi
XX Cell
KW Cance
XX Cunide
XX Unide
XX WO200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, eppilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                  0321/c
ABL70321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising frag
for diagnosis and treatment
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine
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                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                        2953
                                                                                                                                                                                                                                                                                                             3013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5914 BP; 1235 A; 162 C; 1616 G;
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                                                                    Cell signalling; cytosine methylation;
                                                                                               Chemically treated cell signalling DNA sequence#106
                                                                                                                                                         ABL70321;
                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                            31 ACACTATCCTTTACCCACGCTCAACAGTTTAATAACCTGCCAGCAATAAGGGATGTTGTT 90
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                                                                                                                                                                                                                                                       TCCAACCCAAAAATACAAACGTATTTACATCTAAAATACGTATCCCC
                                                                                                                                                                                                                                                                                CTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCC
                                                                                                                                                                                                                                                                                                            TACCCTCTATAAAATAATTTCTTAACAAACCCACGAATACAATATACCGCTCGAAAAAAT 2954
                                                                                                                                                                                                                                                                                                                                                                   AAACTCCCATTCACACACGTCAATCAATTTAAAAAACCAAATACCTTTTATCCAATCAATC 3014
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                         tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2141; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methylation
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                                                                                                                                                                                     standard;
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2000DE-1043826
                                                                                                                             (first entry)
                                                       cytostatic;
                                                                                                                                                                                     DNA;
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                                                                                                                                                                                     6310 BP
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Pred. No. 2.
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                                                                         cell signalling disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the cinvention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences genomic DNA's of genes associated with cell signalling. The through DNA's of genes associated with cell signalling. The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
      cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid, useful with cell signalling sequences of genes as
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       TCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCTGAAGTTAATG
                                                                                                                               gene regulation-associated gene oligonucleotide #223.
                                                                                             Gene regulation-associated gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , useful for diagnosis and therapy of diseases associated gnalling e.g. cancer, comprises chemically modified genom genes associated with cell signalling .
                                                                                                                                                            (first entry)
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Pred. No. 2.5;
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212

GATCAATCAAGAGAGA 227

TAAAAAAATATCAAAACTTAATATTAAAAAAAAATAACGAAAAAACCTCAATAATTAAATA

Gaps

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2390 151

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В

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Search completed: February Job time: 1034 secs

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer. Merner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rne invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissipation to the complementary to contact the complementary sequences.
                                                                                         2449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
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01-SEP-2000;
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07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                              Sequence 6310 BP; 1426 A; 213 C;
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TCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCCTGAAGTTAATG
                                                                                         EPIGENOMICS AG
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    GenCore version Copyright (c) 1993 - 2003
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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US-08-459-415-1
US-09-066-687-1
US-09-066-687-2
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US-08-821-944-65
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APPLICANT: Lodes, Michael J.
APPLICANT: Lichem, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEO ID NOS: 334
SOFTWARE: PASTSEQ for Windows Version 3.0
SEO ID NO 272
LENGTH: 443
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
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US-09-397-787-272
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                        Sequence 3, Application Patent No. 5976837 GENERAL INFORMATION:
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                                                                                                                          327 TAAATACATTTGAGGGGT 344
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74; Conservative
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Jacobs, Kenneth McCoy, John M.
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53.6%;
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US-08-617-053A-3
US-08-687-080-55
US-08-973-273-4
US-09-134-001C-1302
US-07-961-522-3
US-08-321-74.88-3
US-08-321-978-3
US-08-710-884-3
US-08-731-272A-29
US-08-731-272A-29
US-08-731-272A-29
US-09-134-001C-2222
US-09-022-699-3
US-09-022-699-1
US-08-455-968E-4
US-08-455-968E-4
US-08-455-968E-4
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> Treacy, Merberg, Racie, Lisa LaVallie, Edward

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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Olszew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                      APPLICANT: Torbert, K. TITLE OF INVENTION: SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                    3660 CAATTTTTGAAATTAAAAAAGTTGAGAATCTTGAAA 3625
                                                                                                                                                                                                                                                                                                                                                                                                                  3720 AAAAGAGTTCTTATTCTCCCAAAATAGGAAATTTTGTATTCCTATAGTCAAAACAATAAA 3661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                 113 GAATTTTCCAACGAACAAAAGCTAAATATCGCAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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                                           CITY: Minneapolis
                                                             STREET:
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              COUNTRY:
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                                                             E: Schwegman, P.O. Box 2938
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4078 base pairs
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Agostino, Michael J.
ENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
VENTION: ENCODING THEM
             USA
                                                                                                                                                                                      Tzafrir, I.
Somers, D. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                        Olszewski, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                       Lockhart, B.
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                                                                                                                           PROMOTER
                                                                                                                                          SUGARCANE BACILLIFORM VIRUS
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                                                                            Woessner & Kluth, P.A.
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                                                             , ORGANISM: sugarcane bacilliform virus US-09-349-546-2
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                                                                                                           SEQ ID NO 2
LENGTH: 7568
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APPLICANT: Somers, D.A.
APPLICANT: Lockhart, B.
APPLICANT: Torbert, K.
TITLE OF INVENTION: Sugarcane bacilliform virus promoter
FILE REFERENCE: 600.369US2
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/349,546
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: US 08/694,869
EARLIER FILING DATE: 1996-08-09
EARLIER APPLICATION NUMBER: PCT/IB97/01338
EARLIER FILING DATE: 1997-08-13
                                                                                                                                           NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olszewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              TYPE: DNA
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APPLICATION NUMBER: US/0
FILING DATE: 09-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5962 AACATATTAATAAGAAGATTGCAGAATTTGATGACGAGAAGTTGAAGACAAAAGAAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GAATTTTCCAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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SOFTWARE: FastSE
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REGISTRATION NUMBER: 30,440
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5. 6093569
                Similarity
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Score 32.4; DI
Pred. No. 2.9;
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Pred. No. 2
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                                                                  US-08-459-415-1
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            Sequence 1, Application US/08459415 Patent No. 5744334 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dobres, Michael S. and Mandaci, Sevnur TITLE OF INVENTION: A Plant Promoter Useful for Di
                                                                                                                                                                                                                                                                   1089 TATATCATAATATAAATCATTTTACAATGTTTAAAAAGAATTAATATTAGTTTTTTTATTAT 1148
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL:
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   APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                    89 TTTAACTTAAGTCAAAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAA 148
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les 77; Conserv
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                                                                                                                                                    ATGGATCAATCAAGAGAGATGTGGGCTGTAAT 240
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 Dobres, Michael S.
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and Mandaci, Sevnur
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Plant Epidermis
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us-09-066-687-1
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US-08-459-415-1
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                                                                                                                                                                                                                          GENERAL
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                 APPLICANT: Dobres, Michael S. and Mandaci, Sevnur
TITLE OF INVENTION: Expression of Foreign Proteins to the Plant Epidermis
                                                                                                                                                                                                                                                                                                                                                                                                                                1149
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HYPOTHETICAL:
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NAME: Beardell, Lori Y.
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PRIOR APPLICATION NUMBER:
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OPERATING SYSTEM:
                                                                  STREET: One LIDELLY
CITY: Philadelphia
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                                                         STATE:
                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place 46th. Floor
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                                                                                                                                                                                                                          INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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Plant Epidermis
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Best Local :
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LENGTH: 2861 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                   FILING DATE: September 2, ATTORNEY/AGENT INFORMATION: NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET; One Liberty Place 46th. Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dobres, Michael S. and Mandaci, Sevnur TITLE OF INVENTION: A Plant Promoter Useful for Directing the Expression TITLE OF INVENTION: of Foreign Proteins to the Plant Epidermis
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                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTUANED: TOTAL
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les 77; Conserv
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                                                                                                                                              CLASSIFICATION:
                 REFERENCE/DOCKET NUMBER:
                                REGISTRATION NUMBER: 34,293
                                                                                                                                                               FILING DATE:
                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                      APPLICATION NUMBER:
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INFORMATION:
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                                                                                                        08/299,953
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                 NOVA-0016
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US-08-299-953-2
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US-08-299-953-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL:
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                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                             HYPOTHETICAL:
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                 ANTI-SENSE:
                                             MOLECULE TYPE:
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STATE: F..
TD: 19103
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                                                                              TENGTH: 3881 Land mype; nucleic acid
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                                                             TOPOLOGY:
                                                                        STRANDEDNESS:
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                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                               REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herew
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215-568-3439
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A Plant Promoter Useful for Di
Expression of Foreign Proteins
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Pred. No. 2.4;
0; Mismatches
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Plant Epidermis
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Query Match

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Score 32;

DB 1;

Length 3881;

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                  149
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STATE: FA
TO: 19103
PEAD/
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CITY: Philadelphia
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                                                                                                                                 Local Similarity 50.7 ies 77; Conservative
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STREET: One Liberty Place 46th. Floor
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                  ACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCCTGAAGTTA 208
                                                                                       TTTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAA 148
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TATATCATAATATAAATCATTTTACAATGTTAAAAAGAATTAATATTAGTTTTTTATTAT
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                                                                                                                             Score 32; DB:
Pred. No. 2.8;
0; Mismatches
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Plant Epidermis
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                                                                                        RESULT 12
PCT-US95-11231-2
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Patent No. 6339185
                                                     Sequence 2, Application PC/TUS9511231 GENERAL INFORMATION:
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                                                                                                                                                                                                                                 1149
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
APPLICANT: Dobres, Michael S. and Mandaci, Sevnur TITLE OF INVENTION: A Plant Promoter Useful for Directing the Expression TITLE OF INVENTION: of Foreign Proteins to the Plant Epidermis
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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STATE: 19103
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                               ACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCCTGAAGTTA 208
                                                                                                                                                             ATTAATATAAAAGATATTTTTTTGATATAAT 1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3881 base pairs
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Pred. No. 2.
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2.8;
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ins to the Plant Epidermis
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US-08-341-568-1
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                                                                                                                                                                                                                                                                Sequence 1, Application US/08341568 Patent No. 5661021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11231
FILING DATE: Herewith
CLASSIFICATION:
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FILING DATE: September 2,
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-564-8960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Woodcock Washburn Kurtz Mackiewicz & Norris STREET: One Liberty Place 46th. Floor CITY: Philadelphia STATE: PA ZIP: 19103
                                                                                           APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranua
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods
TITLE OF INVENTION: pulps
                                                                                                                                                                                                   APPLICANT:
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                                                                           CORRESPONDENCE ADDRESS:
                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3881 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NOVA-0016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
COUNTRY:
                             CITY: Falls Church
                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                  ATGGATCAATCAAGAGAGATGTGGGCTGTAAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCTGAAGTTA 208
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                                            3: Birch, Stewart, Kolasch and Birch
PO Box 747
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Viikari, Liisa
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50.7%;
                                                                                                                                                                                                                                    Johanna
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ber 2, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.6%;
Best Local Similarity 50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 36:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF THE TENDENMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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NAME: Murphy Jr, Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 APPLICANT: Saloheimo, Anu APPLICANT: Marjatta, Ranua APPLICANT: Marjatta, Ranua TITLE OF INVENTION: Mannanase enzymes, genes coding for them, TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching TITLE OF INVENTION: lignocellulosic pulps
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 АЛЛАНААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАСТСGAG 536
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TELEFAX: (703) 205-8050
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                                                                          COUNTRY: US
ZIP: 22040-0747
                                                                                                                   CITY: Falls Church
STATE: VA
                                                                                                                                                          ADDRESSEE: Birch, Stewart, STREET: PO Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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nucleic acid
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Viikari, Liisa
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SYSTEM: PC-DOS/MS-DOS
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    Mismatches

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                                                                                                                                                                              Kolasch and Birch
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

CLASSIFICATION:

APPLICATION NUMBER: FILING DATE: 13-AUG

NUMBER: US/08/911,020 13-AUG-1997

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1446)
US-09-135-639-1
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US-09-135-639-1
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                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1449
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: DALFON MICHAEL A.,
APPLICANT: WILSON, GEOFFREY G.
APPLICANT: WILSON, GEOFFREY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
 Best Local Similarity
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09135639 Patent No. 6004793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                          TITLE OF INVENTION: Method For Cloning And Producing The Aval Restriction TITLE OF INVENTION: Endonuclease In E. coli and Purification Of The TITLE OF INVENTION: Recombinant Aval Restriction Endonuclease FILE REFERENCE: Aval Recombinant Aval Restriction Endonuclease CURRENT APPLICATION NUMBER: US/09/135,639
CURRENT FILLING DATE: 1998-08-18
CURRENT FILLING DATE: 1998-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                             ORGANISM: Anabaena variabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
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ORIGINAL SOURCE:
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LENGTH: 536 base pairs
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REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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nes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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STRANDEDNESS: single
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6.6%;
54.8%;
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Pred. No. 1.3;
0; Mismatches
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Score 31.8; DB 3; Pred. No. 2.1;
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               Length 1449;
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Db 462 AAAACCTTGGAATCAGCATAATAATAGAAAATATCTTAATCGTTTAAGAATTACTGACG

522 AGCTTATCCTCCTGAAACAGAAGCATCAATAGAGAGAGTTTTTATTTTCTATAGAA 576

Search completed: February 7, 2003, 21:13:45
Job time: 104 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 7, 2003, 19:42:18; Search time 98 Seconds (without alignments) 2326.484 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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   US-09-828-456-1
US-09-938-842A-3476
US-09-938-842A-792
US-09-9876-889-272
US-09-880-107-3768
US-09-880-107-3768
US-09-880-107-3814
US-09-9880-107-3814
US-09-988-44A-3316
US-10-098-841-110
US-10-098-841-110
US-10-098-841-110
US-09-925-302-117
US-09-960-352-7904
US-09-960-352-7904
US-09-9764-853A-2
US-09-754-853A-3
US-09-754-853A-3
US-09-754-877-914
US-09-938-842A-5219
US-09-938-842A-5219
US-09-938-842A-5219
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Sequence 1, Appli
Sequence 3476, Ap
Sequence 5260, Ap
Sequence 792, App
Sequence 272, App
Sequence 3768, Ap
Sequence 316, Ap
Sequence 3110, App
Sequence 110, App
Sequence 170, App
Sequence 7904, Ap
Sequence 2763, Ap
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5219, Ap
Sequence 5219, Ap
Sequence 1, Appli
Sequence 48, Appli
                                                                                                                                                                                                                                                                                                                Description
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US-09-828-456-1
Sequence 1, Application US/09828456
Patent No. US20020051982A1
Patent No. US20020051982A1
GENERAL IMPORMATION:
APPLICANT: Levy, Stewart et al.
TITLE OF INVENTION: No. US20020051982A1e1 BLR Molecules Affecting Antibiotic Suscential Reference: pKZ-030
CURRENT APPLICATION NUMBER: US/09/828/456
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,505
PRIOR APPLICATION NUMBER: 60/218,380
PRIOR APPLICATION NUMBER: 60/218,380
PRIOR FILING DATE: 2000-07-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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; LOCATION: (239)..(361)
US-09-828-456-1
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                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 481; Conservative 0
                                                                                                                                                                                                                                                                                                                             LENGTH: 481
TYPE: DNA
ORGANISM: Escherichia c
FEATURE:
                                                121 CAACGAACAAAAGCTAAATATCGCAAAAAACCTCAGTAAAAAATCTTGCTGGAGCTAITATT 180
   61
                                                                                                                                                       AATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTC 120
                                CAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATT
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10 US-09-764-847-1425

110 US-09-867-701-7321

110 US-09-960-352-5785

110 US-09-960-352-5785

110 US-09-960-352-300-719

110 US-09-349-385-3

110 US-09-349-385-3

110 US-09-815-048-1

110 US-09-815-048-1

110 US-09-815-048-1

110 US-09-88-842-2799

110 US-09-98-842-2799

110 US-09-98-842-2799

110 US-09-98-617-1

110 US-09-98-1-1

110 US-09-98-1-1

110 US-09-98-1-1

110 US-09-70-689-3

110 US-09-833-381-1132

110 US-09-98-598-454

112 US-10-001-870-42

113 US-09-70-870-43

114 US-09-74-592-3

115 US-09-70-9874-592-3

116 US-09-70-9874-592-3
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Pred. No. 5.3e-131;
0; Mismatches 0;
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                                                                                                                                                                                                                                                   Length 481;
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Minimum DB Maximum DB

seq length:
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Scoring table: Sequence:

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Perfect score:

US-09-828-456-1 481

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6 0 10 10 10 10 10 10

481 1947 7053 66109 198285 2000 2075 2075 4083 335913 335913 335913 683 683 683 7200

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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STARESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT EILING DATE: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR SEQ ID NO 3476
LENGTH: 1947
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-3476
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Best Local
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                                                                                                                                                                                                                                 16 TATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTTAATAACCTGCCAGCA 75
                                                                                                                                                                                                                                                                                Local Similarity
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                            CCCCCTGAAGTTAATGGATCAATCAAGAGAGAT 228
                                                                  TAATATCACTTTAGTTTTTTACAAATAATGATTTGAGTATAATTTGATCGTAATTTGTA
                                                                                                AAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTA 195
                                                                                                                                   TTCAAAGTAATTTTTGGATTCACATCACCAAAAAAATTAACAGAACAGAGTTAACCACGT
                                                                                                                                                                 ATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAACAAAAGCT 135
                                                                                                                                                                                                   TATGATTGTTTATAGTTTCCGTTCATCATCAACTTTAAACTTTTAATTGTACGAGAAACT 907
ACCCCATTTCATCATGGAAACAACAATAAAGTT 754
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                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                  48.8%;
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CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 5260
LENGTH: 332
TYPE: DAA
ORGANISM: Bos taurus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: US-09-983-965-5260
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                                                                                                                                            ; NAME/KEY: SITE
; LOCATION: (154)
; OTHER INFORMATION:
US-09-764-864-792
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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5260, Application US/09983965 Patent No. US20020137160A1
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                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Byatt, John G.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
                                                                       Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Warren,
                                                                                                                                                                                                                 LENGTH: 7053
TYPE: DNA
ORGANISM: Homo s
FEATURE:
                                                                                                                                                                                                                                                                                                                         Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
3528 TTAACTTTTGTGAAAATAATACCTAAGGTTTTCTGGCTTATTGAGGAAATTTCCTAACAA 3469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AAATTAAATTCATCTTACTCAAGAAAATATTATAAACAAAGTAAACATTTAAGCCAAATA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAAAACCTCAGTAAAAAT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 TTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAACA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATTAGAGAGTTTTATGTGATCACCTACTGTAATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                792, Application US/09764864
                                                                         66;
                                                                                        Similarity
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                                                                                        Score 36.8; DB 10; Pred. No. 0.79;
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CCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCTGAAGTTAA

209

ACAAACAAACAAACAAACAGAAGAGAAGATCATTAACCACTGTATACTTTGTGTATATAA 3409

257

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; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-889-272
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APPLICANT: Horne, Da
APPLICANT: Vockley,
APPLICANT: Scherf,
APPLICANT: Gene Log
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LENGTH: 443
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Best Local
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                               CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                  APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
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SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/876,889
SOFTWARE: Pat
EQ ID NO 3768
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ORGANISM: Homo sapien
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAAAAATAGCGAATTTTCCAACGAACAAAAGCTAAATATCGCAAAAACCTCAGTAAA 159
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                   PatentIn
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King, Gordon E.
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53.6%;
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; OTHER INFORMATION: n = US-09-880-107-3768
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LENGTH: 198285
TYPE: DNA
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Best Local Similarity
Matches 101; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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                                                                                                                                                         89480
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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89600 TGGAAATATAGGAGAAATTACTCTCAGAGATATGATGTTATTTAAGTCATTGACATATTG 89659
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                                                                                                   GCAATAAGGGATGTTGATTTAAGTTAAGTCAAAAAAATAGCGAATTTTTCCAACGAACAAAA 132
                                                                                                                                                       AAGGATTATTCTTAATTCCTGCCTTCCTTTCTAAATCCCCAATCCTCAATTGAACTCTTTA 89539
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                                     GCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACAT 192
                                                                           ATTATATTTCCTGTTTATTTATTGAATGGAAAAATGGAAAATTATCTAACATTTGTCA
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                                                                                                                                                                                                                                 101;
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Pred. No. 7.3;
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3316
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PRICING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3316
LENGTH: 1512
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APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 859, Application US/09887576 Patent No. US20020144047A1
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APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, B.
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                   PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
                                                                                                                                            APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89660 TTAACCTCAGATGCAAATGGTGGAATTAATA 89690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 51.7 es 78; Conservative
FILING DATE: 200
R OF SEQ ID NOS:
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                                                                                                                                                                                                                plant expression
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; ORGANISM: Oryza
US-09-887-576-859
                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (147)..(2075)
US-10-098-841-110
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US-10-098-841-110
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
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SEQ ID NO 859
                                                                                                                                                                                                                                                                                                 SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 110
                                                                                                                               Query Match 7.1%;
Best Local Similarity 50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 110,
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                 ENGTH: 2075
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116 TTTTCCAACGAACAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTA 175
                                               499 ATTTTAGAAATGACTCAGAATATAGACAATTTGAGGGACTACAGGGATATCAAGAAGGAA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 TIGTTTAACTTAAGTCAAAAAAATAGCGAATTTTTCCAACGAACAAAAGCTAAATATCGCA 145
                                                                              AATTATTCAATTATAGATTTAATAAAACTATGCTGGTGTTGTAAATATTAC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGACTAATTTTTTAGAAAAAAATAGTAAATTTTTTAACCGAAGACAAATATATTATGAAA 548
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Chen, Rui-hong
Wang, Dunrui
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Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Zhiwei
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, Chongjun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi, Vinod
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Pred. No. 2
                                                                                                                                  Score 34.2;
Pred. No. 2
                                                                                                                  Mismatches
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                                                                                                                                                    Length 2075;
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; LOCATION: (157)
; OTHER INFORMATION: n equals a,t,g,
US-09-925-302-177
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                                                                                                 APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
CURRENT FILING DATE: 2001-09-24
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                                                                     SEQ ID NO 7904
LENGTH: 241
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OTHER INFORMATION: -09-960-352-7904
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                             APPLICANT: Warren, Wesley C.
   TYPE: DNA
ORGANISM: Bos taurus
ORGANISM: Clone ID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GAATTTTCCAACGAACAAAAGCTAAATATCGCAAAA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AACAGTTTAATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGC 112
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les 57; Conserv
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               34-LIB3057-019-Q1-K1-A10
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Pred. No. 5.3;
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; TYPE: DNA
; ORGANISM: HOMO
US-09-867-701-2763
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US-09-867-701-2763
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CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2763
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09754853A Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2763, Application US/09867701 Patent No. US20020132237A1
                                                                                                                                                     SEQ ID NO 2
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                                                                                                                                                                                     APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1119
NAME/KEY: CDS
LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
OTHER INFORMATION: Clone ID: 240017_region_G3
                                                                   ORGANISM: Glycine max FEATURE:
                                                                                                              TYPE: DNA
                                                                                                                               LENGTH: 335913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ATTTTCCAACGAACAAAGCTAAATATCGCAAAAACCTCAGTAAAAA 161
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57.0%;
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Pred. No. 2.8;
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Pred. No. 1.7;
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 3
LENGTH: 335913
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 311248 TTTAAATTAATAAGTTATATACCAACAATATAAAACATACAAGTTTATAATATCATCTGA 311189
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Db 311308 AAATAAAAAAATAATTTTACAACAACTAAAAGCAAAAAATATCTAAAGACTAAAGAAATA 311249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS; LOCATION: (46798)..(48763)..(48975)...(49573); OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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US-09-754-853A-3/c
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Search completed: February 7, Job time: 334 secs
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Best Local Similarity 50.3%;
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%; Score 33; DB 9; Length 335913; Best Local Similarity 50.3%; Pred. No. 57; Matches 81; Conservative 0; Mismatches 80; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                           311188 TGATAAATTAGTATCTAATAAATTTATTAACTTTTATAATA 311148
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Maximum Match 100%
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Perfect score:
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41.8
41.6
41.2
40.2
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seq length:
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Match
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AA572059 vk95d03.r
AV846478 AV846478
AV861290 AV861290
AL105557 Drosophil
BJ364861 BJ364861
AV867201 AV867201
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AA/00428 ZJ/4d10.8		AI802215 th36b06.x	AI423972 tf36q07.x	AA912460 om52c06.s	AI985789 wt20f04.x	AI818334 wk59d01.x	AI768981 wg31c03.x	AI140942 qa83h02.s	AA983620 on44b02.s	AA664128 ac06c07.s	AI361450 qy43e11.x	AW576565 UI-HF-BNO	H54495 yq89f08.rl	AI419275 tf21h04.x	AI291645 qm85c07.x	AW515536 xx66f07.x	AI383833 tc99c03.x	AL059446 Drosophil	BG434608 602506674	AW180813 MgA0974f	вJ368191 вJ368191	AQ181233 HS_3216_B	вQ601966 мІ-Р-ЙО-а	AL061385 Drosophil	AZ660149 1M0538L02	AV404587 AV404587	AZ534410 ENTBR77TF	V7219	B631]	NTNR	H230-	R2-CT(NTEM44T	NTRX	J3701	1c05.	0127831	M0083	88 ENTPNO9T

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ALIGNMENTS

REFERENCE AUTHORS SOURCE ACCESSION VERSION KEYWORDS RESULT 1 AA572059/c COMMENT DEFINITION TITLE JOURNAL Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 672)

1 (bases 1 to 672)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R. AA572059 672 bp mRNA linear EST 27-AGC-1997 vk95603.rl Knowles Solter mouse blastcoyst B1 Mts musculus cDNA clone IMAGE:962405 5' similar to SW:YHHX_ECOLI P46853 HYPOTHETICAL 38.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION ;, mRNA sequence. EST Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the The WashU-HHMI Mouse EST Project house mouse. AA572059.1 GI:2345254 Louis, MO 63108 EST 27-AUG-1997

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RESULT 2
AV846478
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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KEYWORDS
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                                   Local Similarity
nes 118; Conser
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ATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCACGCTCAACAGTTTAATAACCT 68
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l Similarity 100.0%;
45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV846478 Nori Satoh unpublished cDNA library, cleavage stage embryo Ciona intestinalis cDNA clone rcicl16110 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciona intestinalis
                                                                                                                                                                                                                                                                                       Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                         Satoh, N., Satou, Y., Kohar Expressed genes in Ciona Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phlebobranchia; Cionidae; Ciona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger Inserts) and B3."
                                                                                                                /tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/note="Vector: pBluescript SK"
87 c 104 g 203 t 1
                                                                                                                                                                                      stage embryo"
                                                                                                                                                                                                      /organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="rtoilifil0"
/clone_lib="Nori Satoh unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Knowles Solter mouse blastocyst
/tissue_type="blastocyst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:962405"
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Pred. No.
                                 Score 41.8; DI Pred. No. 0.99 O; Mismatches
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ACATTTACCCCCTGAAGTTAATGGATCAATCAAGAGAGATGTGGGCTGTAATGAATCGTC
                                              AAATTCTAAATTTGGTACAATGTGTGCATTTATTCCGATTGAATGTTTCAGTTCAAGAAA
                                                                AAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTA 188
                                                                                                             GGCAGTATACAAGCAAATTTGCAAATTGATTACACCAATACACCATTATACAAAATGAAA
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Department of Zoology
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Expressed genes in Ciona intestinalis
Unpublished (2000)
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Sakyo-kw, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: satoh@ascidian.zool.kyoto-u.ac.jp
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/clone="rcleg34e21"
/clone=lb="Nor1 Satoh unpublished cl
/tissue_type="whole animal"
/dev_stage="egg"
/dev_stage="egg"
/note="vector: pBluescript SK"
a 101 c 122 g 242 t 10 ot
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Pred. No. 1;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomi
AL105557
AL105557.1
 BJ364861 407 bp mRNA linear EST 08-MAR-20
BJ364861 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc33c11 5', mRNA sequence.
BJ364861
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pBeloBAC11.
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/note="end : T7"
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Pred. No. 1.1;
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Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                 Kyoto University
Sakyo-ku, Kyoto, Kyoto
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                  Contact: Nori Satoh
Department of Zoology
                                                                                                                                   Phlebobranchia; Cionidae; Ciona.

(bases 1 to 501)
Satch, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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EST.
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Urochordata;
                                                                                                                                                                                                                                                                           AV867201.1 GI:16854725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
Email: satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:44689"
/clone="ddc33c11"
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64 c 29 g 108 t
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Pred. No. 1
                                                 606-8502,
                                                 Japan
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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 GCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGCGAATTTTCCAACGAAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 ATTGAAGTATGATGGCTATTTTGACACTATCCTTTACCCACGCTCAACAGTTTAATAACCT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAGCTAAATATCGCAAAAACCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAGTATACAAGCAAATTTGCAAATTGATTACACCAATATACCATTATACAAAATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTTACCCCCTGAAGTTAATGGATCAATCAAGAGAGATGTGGGCTGTAATGAATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTCTAAAATTGGTACAATGTGTGCATTTATTCCGATTGAATGTTTCAGTTCAAGAAA
                                                                                                                                                                                                                   Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 343
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                        Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 940)
1 (bases 1 to 940)
1 Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
1 Determination of clone end sequences from Entamoeba histolytica
HM1:MSS sheared DNA library (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
                                                                                                  High quality sequence start: 15
High quality sequence stop: 703
Location/Qualifiers
                                                                                                                                                     DNA library
Seq primer: Ml3-Forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Entamoeba histolytica.
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BH146288
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                                                                                                                                                                                                         Clones are derived from
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/tissue_type="whole animal"
/dev_stage="egg"
/note="Vector: pBluescript SK"
/note="Vector: pBluescript SK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="rcieg50106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:7719"
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/clone_lib="Entamoeba
/note="Vector: pHOS1;
                                  /strain="HM1:IMSS"
/db_xref="taxon:5759"
                                                                  organism="Entamoeba histolytica"
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47.8%;
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Pred. No. 2.
                                                                                                                                                                                                         the Entamoeba histolytica HM1: IMSS sheared
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histolytica
Site_1: Bst
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6
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 Sheared DNA"
I; Constructed
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   at The
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RESULT 8
AZ347477
LOCUS
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AUTHORS
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ORGANISM
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                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 GTAATTTCTTACAACAAAAAAAAGAAAACCATGAGTTTTTGATTAAATATTGGATAATTG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 TGAAGTTAATGGATCAATCAAGAGAGATGTGGGCTGTAATGAATCGTCTTATTGAATTAA
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                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0083 row: 0 column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 663)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ347477 663 bp DNA linear GSS 29-SEP-200 IMM0833005R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0083005 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Murldae; Murlnae; Mus
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                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B.
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                                                                                                                                            quality sequence stop: 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S.
                                   /organism="Mus musculus"
                                                                                                     Location/Qualifiers
/strain="C57BL/6J"
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49.7%;
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Pred. No. 5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 TGGCTGTTATGCTGTCACTTGTAACTCAAGACCTTGGTTATCATATGGAATTGTGTTGCA 531
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 891)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE531179 891
601278311F1 NIH_MGC_39 Homo
                                                                                                                                         Tissue Procurement: ATCC
                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE531179.1 GI:9759915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              numan.
                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AFT2970721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone="uugC1M0083005"
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Pred. No. 9.2;
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IMAGE:3610347 5',
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                                                                                                                                                                                                                                                          76;
                                     Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2214 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 2214
High quality sequence stops: 210
                                                                                                                                                                      4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
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IMAGE:241448 5', mRNA sequence.
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                                                                                                                                                                                                                         Washington University School of Medicine
                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                        Unpublished (1995)
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                             quality sequence stop: 210
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/lab_host="pHIOB (phage-resistant)"
/lab_host="pHIOB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming the following 5' adaptor: GGCACGAG(G). Library construct by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Liff Technologies)."
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           Location/Qualifiers
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54.7%;
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Pred. No. 9.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGGTCAGTGTANAGANATATGATTTGAGGTGGTGCATGCAAGTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCAGTAAAAATCTTGCTGGAGCTATTATTGCTAAGTAACATTTACCCCCTGAAGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ370199 633 bp mRNA linear EST 08-MAR-2
BJ370199 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc53c12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                      Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                              Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                   Urushihara,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:3790581"
/db_xref="taxon:9606"
/clone="IMAGE:241448"
                                                                                                                       /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc53c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares fetal liver spleen lNFLS"
                                                    /dev_stage="Culmination stage" 73 c 116 g 217 t
                                                                                                      /clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                     /sex="mat A"
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   7.98;
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   Score
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   38;
   DB
   13;
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Length 633;
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RESULT 12
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 TTAATAAATAATTGGGCAGGATCAAGTGGCACATATTTTAGTGGTTGGGG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 TTACCCCCTGAAGTTAATGGATCAATCAAGAGAGATGTGGGCTGTAATGAATCGTCTTAT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 TGAATTAACAGGTTGGATCGTTCTTGTCGTTTCAGTCATTCTTCGTGGCG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 GCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAATAGGGAATTTTCCAACGAACAAAA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Brendan J Loftus
Department of Eukaryotic Genomics
Department of Fukaryotic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic, DNA sequence.
BH161244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 864)
Loftus, B., Wang, Z., Van Aken, S. and Fraser
Determination of clone end sequences from
HM1:IMSS sheared DNA library (2001)
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quality sequence stop: 7
Location/Qualifiers
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301 838 3543
                                                                                                                                                                   G.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450. The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                     /db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone="Vector: pHOSI; Site_L: Bst I; Constructed at The
/note="Vector: pHOSI; Site_L: Gonstructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
using a method described by Clark and Diamond (Clark,
                                                                                    whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."

94 c 99 g 330 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Entamoeba histolytica"
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                         Length 864;
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RESULT 13
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Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       672 TTTTTAGTTAATGGTTTCTTTTATAAATTGATTTGAGAATT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GCTGTAATGAATCGTCTTATTGAATTAACAGGTTGGATCGTT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 GTTTTAAAACACAATAATTATTTCTTTGCTTTTTAAAAGTCTTGAATGTGAGTTATATGA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 ATAATTTTATTATAATTATTAAATTTTATATTATAAAACAAAGTAAAAATTAACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AACAGTTTAATAACCTGCCAGCAATAAGGGATGTTGTTTAACTTAAGTCAAAAAAATAGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAATGAAATACTTTTCAAATGAACAAATAAACGAATCAAATAAAAAACAAAAAAATAAT 551
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AZ547495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determination of clone end sequences HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 949)
Loftus,B., Van Aken,S. and Fraser,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Entamoebidae; Entamoeba
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301 838 3543
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     Conservative
                                                                                                                                                                                  Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence.
                                                                                    whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
113 c 115 g 361 t
                                                                                                                                                 the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                   /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                           /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                   7.98;
pred. No. 11;
0; Mismatches
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11;
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                                 Length 949;
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MEDLINE
Query Match
Best Local Similarity
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370 ATAATTTATTATAATTATTAAATTTTATATATATAAAACAAAGTAAAAAATTAACAAGAA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGTAATGAATCGTCTTATTGAATTAACAGGTTGGATCGTT 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 485)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF083668 485 bp mRNA linear EST 18-OCT-200 MR2-CT0456-130900-001-h12 CT0456 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson, A.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR2-CT0456-130
900-001-h12&t3=2000-09-13&t4=1)
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                                                                                                       /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196: 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:960|
/clone_lib="CT0456"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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7.9%;
Score 37.8;
Pred. No. 12;
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                              DВ
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                           Length 485;
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ACCESSION
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BH288998
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Best Local Similarity
Matches 105; Conserv
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78
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TCAAATTCAATTTTATTCATAACAAATACATTTTATAACACAAAAGGATTAAAAATGACT 137
                                  TCTCATTGAAGTATGATGGCTATTTGACACTATCCTTTACCCCACGCTCAACAGTTTAATA 64
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
nia+a. 2 row: L column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH230-2L9.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-2L9, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., c
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-2L9.TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: T7
Class: BAC ends
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                                                                         Conservative
                                                                                                                                                              /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced Pleter de Jong" 86 g 145 t
                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                           cell_type="Brain"
                                                                                                                                                                                                                                                                                  /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                     /clone="CH230-2L9"
                                                                                        7.98;
                                                                       ; Score 37.8; D; Pred. No. 12; 0; Mismatches
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                                                                                                              Length 513;
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Search completed: February 7, 2003, 21:11:55
Job time: 2449 secs